SEQUENCE LISTING

<110> Cahoon, Rebecca E.
Falco, Saverio C.
Kinney, Anthony J.
Miao, Guo-Hua

<120> Plant Polyphenol Oxidase Homologs

<130> BB1330

<140> 09/889,463
<141> 2001-07-16

<150> 60/119,590
<151> 1999-02-10

<160> 46

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<213> Zea mays

<220>
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<223> n = a, c, g or t

<220>
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gtgcgcatct cccagaggcg aacgctccga gccagacgcc caaaagcacg accgccgcga 180
cgtcctcctc ggcctcggag cgctcggtgc cagtgccacc gctaccctgg cgtccgcgcg 240
ccgcgccggc gccgaccccg tcgccacgcc cgacatctct tcctgcggcc aagcgaacct 300
tccggtgagc gccaacgtgc tgacgtgctg cccgccgccc tcgagcgcgc tgcccgtgga 360
cttcatcctc cccgacgcca cgtccttgcc gctccggacg cgccccgccg cgcactcggt 420
caccacggac tacgtcgcca aagttcaacg ccgggatcgc tgcgatgaag gggctcccgg 480
cgggacganc cgcgtagctt cgcggcgcan gg 512

<210> 2
<211> 150
<212> PRT
<213> Zea mays

<400> 2
Met Ala Ser Ile Ser His Leu Ile Ala Lys Pro Ala Pro Ala Ala Thr
1 5 10 15

Phe Pro Leu Ser Leu Pro Arg Thr Ser Ser Gly Phe Arg Pro Arg Arg
20 25 30

Val Thr Val Gln Arg Val Ser Cys Ala Ser Pro Arg Gly Glu Arg Ser

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         35                  40                  45

Glu Pro Asp Ala Gln Lys His Asp Arg Arg Asp Val Leu Leu Gly Leu
     50                  55                  60

Gly Ala Leu Gly Ala Ser Ala Thr Ala Thr Leu Ala Ser Ala Arg Arg
 65                  70                  75                  80

Ala Gly Ala Asp Pro Val Ala Thr Pro Asp Ile Ser Ser Cys Gly Gln
                85                  90                  95

Ala Asn Leu Pro Val Ser Ala Asn Val Leu Thr Cys Cys Pro Pro Pro
            100                 105                 110

Ser Ser Ala Leu Pro Val Asp Phe Ile Leu Pro Asp Ala Thr Ser Leu
        115                 120                 125

Pro Leu Arg Thr Arg Pro Ala Ala His Ser Val Thr Thr Asp Tyr Val
    130                 135                 140

Ala Lys Val Gln Arg Arg
145                 150
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<210> 3
<211> 995
<212> DNA
<213> Zea mays

<400> 3
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gcgtctcgtg cgcatctccc agaggcgaac gctccgagcc agacgcccaa aagcacgacc 180
gccgcgacgt cctcctcggc ctcggagcgc tcggtgccag tgccaccgct accctggcgt 240
ccgcgcgccg cgccggcgcc gaccccgtcg ccacgcccga catctcttcc tgcggccaag 300
cgaaccttcc ggtgagcgcc aacgtgctga cgtgctgccc gccgccctcg agcgcgctgc 360
ccgtggactt catcctcccc gacgccacgt ccttgccgct ccggacgcgc cccgccgcgc 420
actcggtcac cacggactac gtcgccaagt tcaacgccgg gatcgctgcg atgaaggcgc 480
tcccggcgga cgacccgcgt agcttcgcgg cgcaggcgag cgtgcactgc gcctactgcg 540
acgggtcgta cagccccgag gggttccccg gtgtggagct ccaggtgcac aactcgtggc 600
tctttttccc cttccaccgc tgctacctat acttcttcga gcgcatcctg ggcagcctga 660
tcggcgaccc cggcttcgcg gtaccgttct ggaactggga cgcgccggac gggatgcgca 720
tgccggccat gtacgcggac cggtcatccc agctgttcga tccgcggcgt gacagccggc 780
acgcgccgcc gaagctcatc aatctggact acaacgccaa cgttagggag ccgaggttca 840
cttactaaca acaggttgat cacaacctca gggtcatgta ccgtcaggta attaacaacg 900
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ccaaaactga tcaaaaaaaa aaaaaaaaaa aaaaa                             995
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<210> 4
<211> 278
<212> PRT
<213> Zea mays

<400> 4
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Met Ala Ser Ile Ser His Leu Ile Ala Lys Pro Ala Pro Ala Ala Thr
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Phe Pro Leu Ser Leu Pro Arg Thr Ser Ser Gly Phe Arg Pro Arg Arg
             20                  25                  30

Val Thr Val Gln Arg Val Ser Cys Ala Ser Pro Arg Gly Glu Arg Ser
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```
         35                  40                  45

Glu Pro Asp Ala Gln Lys His Asp Arg Arg Asp Val Leu Leu Gly Leu
     50                  55                  60

Gly Ala Leu Gly Ala Ser Ala Thr Ala Thr Leu Ala Ser Ala Arg Arg
 65                  70                  75                  80

Ala Gly Ala Asp Pro Val Ala Thr Pro Asp Ile Ser Ser Cys Gly Gln
                 85                  90                  95

Ala Asn Leu Pro Val Ser Ala Asn Val Leu Thr Cys Cys Pro Pro Pro
            100                 105                 110

Ser Ser Ala Leu Pro Val Asp Phe Ile Leu Pro Asp Ala Thr Ser Leu
        115                 120                 125

Pro Leu Arg Thr Arg Pro Ala Ala His Ser Val Thr Thr Asp Tyr Val
    130                 135                 140

Ala Lys Phe Asn Ala Gly Ile Ala Ala Met Lys Ala Leu Pro Ala Asp
145                 150                 155                 160

Asp Pro Arg Ser Phe Ala Ala Gln Ala Ser Val His Cys Ala Tyr Cys
                165                 170                 175

Asp Gly Ser Tyr Ser Pro Glu Gly Phe Pro Gly Val Glu Leu Gln Val
            180                 185                 190

His Asn Ser Trp Leu Phe Phe Pro Phe His Arg Cys Tyr Leu Tyr Phe
        195                 200                 205

Phe Glu Arg Ile Leu Gly Ser Leu Ile Gly Asp Pro Gly Phe Ala Val
    210                 215                 220

Pro Phe Trp Asn Trp Asp Ala Pro Asp Gly Met Arg Met Pro Ala Met
225                 230                 235                 240

Tyr Ala Asp Arg Ser Ser Gln Leu Phe Asp Pro Arg Arg Asp Ser Arg
                245                 250                 255

His Ala Pro Pro Lys Leu Ile Asn Leu Asp Tyr Asn Ala Asn Val Arg
            260                 265                 270

Glu Pro Arg Phe Thr Tyr
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<211> 403
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<220>
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ccgctgccct gggctacgcc taccaggacg tcgccctgcc gtggctgaac gccaagccgg 180
ccaaggaggc cgggtctccg gcgcccaccg cgggcgcgct cccggcgaca ctgaaccaga 240
ccgtgcgggt ggccgtgacg cggcccaaga cctcgaggac ccgcaaggag aaggacgcca 300
aggaagaagt gctggtcgtc caagggatcg aaatcgctga ccactcnaac angttcgtcn 360
agttcgactt gttcgtgaac gaatcccaaa acgggggcng nat 403

<210> 6
<211> 126
<212> PRT
<213> Zea mays

<220>
<221> UNSURE
<222> (117)
<223> Xaa = any amino acid

<220>
<221> UNSURE
<222> (120)
<223> Xaa = any amino acid

<400> 6
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1 5 10 15

Asp Ala Ser Phe Leu Phe Tyr Asp Glu Glu Ala Arg Leu Val Arg Val
20 25 30

Arg Val Arg Asp Cys Leu Asp Thr Ala Ala Leu Gly Tyr Ala Tyr Gln
35 40 45

Asp Val Ala Leu Pro Trp Leu Asn Ala Lys Pro Ala Lys Glu Ala Gly
50 55 60

Ser Pro Ala Pro Thr Ala Gly Ala Leu Pro Ala Thr Leu Asn Gln Thr
65 70 75 80

Val Arg Val Ala Val Thr Arg Pro Lys Thr Ser Arg Thr Arg Lys Glu
85 90 95

```
Lys Asp Ala Lys Glu Glu Val Leu Val Val Gln Gly Ile Glu Ile Ala
            100                 105                 110

Asp His Ser Asn Xaa Phe Val Xaa Phe Asp Leu Phe Val Asn
        115                 120                 125
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<210> 7
<211> 711
<212> DNA
<213> Glycine max

<220>
<221> unsure
<222> (573)
<223> n = a, c, g or t

<220>
<221> unsure
<222> (602)
<223> n = a, c, g or t

<220>
<221> unsure
<222> (669)
<223> n = a, c, g or t

<400> 7

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cgtgtctgca gtgtataatg ttccttccaa gtctaccact ctcccttctt ccctgcatcc 180
attttcacaa tcccaatcca ctaaatatag aaaatcaaaa caccatcaca ctcctagagt 240
gacatgtaat agtggaaacc aaaacaaagg agaaaaacca gatattcata tagaacaaag 300
gaggaacatt ctacttggcc taggagggct ttgtggtgct gctactctta acaacaaccc 360
ttttgcattt gctgcgccaa tatctcctcc aagacctaac acatgtggtc caccagacct 420
acctgaaggt gcagaaccca caaattgttg ccccccattt tcatccacca tcatagattt 480
caagtttcct ccttctaaca aacccttgcg tgtaagacca gctgcacatt tagttgacaa 540
aaattatcta gccaaataca aaaaagccat tgncctcatg aaaaattcca gctaacgatc 600
anctatttca tcaacaagca aacgtgcacg cgctatgcac tggttaaatg acaaattggg 660
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<210> 8
<211> 156
<212> PRT
<213> Glycine max

<220>
<221> UNSURE
<222> (153)
<223> Xaa = any amino acid

<400> 8

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Pro Ser Ser Leu His Pro Phe Ser Gln Ser Gln Ser Thr Lys Tyr Arg
             20                  25                  30

Lys Ser Lys His His His Thr Pro Arg Val Thr Cys Asn Ser Gly Asn
         35                  40                  45
```

```
Gln Asn Lys Gly Glu Lys Pro Asp Ile His Ile Glu Gln Arg Arg Asn
     50                  55                  60

Ile Leu Leu Gly Leu Gly Gly Leu Cys Gly Ala Ala Thr Leu Asn Asn
 65                  70                  75                  80

Asn Pro Phe Ala Phe Ala Ala Pro Ile Ser Pro Pro Arg Pro Asn Thr
                85                  90                  95

Cys Gly Pro Pro Asp Leu Pro Glu Gly Ala Glu Pro Thr Asn Cys Cys
            100                 105                 110

Pro Pro Phe Ser Ser Thr Ile Ile Asp Phe Lys Phe Pro Pro Ser Asn
        115                 120                 125

Lys Pro Leu Arg Val Arg Pro Ala Ala His Leu Val Asp Lys Asn Tyr
    130                 135                 140

Leu Ala Lys Tyr Lys Lys Ala Ile Xaa Leu Met Lys
145                 150                 155
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<210> 9
<211> 2485
<212> DNA
<213> Glycine max

<400> 9

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agtcattcgt gtctgcagtg tataatgttc cttccaagtc taccactctc ccttcttccc  180
tgcatccatt ttcacaatcc caatccacta aatatagaaa atcaaaacac catcacactc  240
ctagagtgac atgtaatagt ggaaaccaaa acaaaggaga aaaaccagat attcatatag  300
aacaaaggag gaacattcta cttggcctag gagggctttg tggtgctgct actcttaaca  360
acaacccttt tgcatttgct gcgccaatat ctcctccaga cctaaccaca tgtggtccac  420
cagacctacc tgaaggtgca gaacccacaa attgttgccc cccattttca tccaccatca  480
tagatttcaa gtttcctcct tctaacaaac ctttgcgtgt aagaccagct gcacatttag  540
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ctaacgatcc acgcaatttc atgcaacaag caaacgtgca ctgcgcttat tgcactggtt  660
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atccaacatt tgcccttcca ttttggaact gggatgctcc taagggcatg caacttcctt  840
ccatttatgc agaccccaaa tcacctcttt atgaccctct tcgcaatgcg aatcaccaac  900
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atgatgatag tgttgtggtg acgttggttc cgaggtatgg gaaagggcgt gtccaaattg 1860
gaggcatcaa gatagatctt gttgcagatt aaaaaatatt tatatacttc gactgtttaa 1920
cctcataata atatatatat atatatatat aatgtagttt cttggatttg tgtttgcttt 1980
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tatatgaaaa atgtagtttt tgttatgtat tttccatgag aatcataaga atgtcgctaa 2040
ttgaagtgaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2100
aaaaaaaacc cccgggggggg ggccgggaac aaaatccccc aaaaagagag tcataaaacg 2160
cgcgcacagg ggccgtcttt taaaaacctc gaaagggaaa aaacccgggc gaaacaaaat 2220
aaaaaccctt taaaaaaaac ccccctttcc aaaaggggaa aaaaaaaaaa aaggcccaca 2280
acaatccccc tccaaaaaaa tttgcccacc caaaagggaa aaggagaccc cccctgtagc 2340
ggcaaaaaaa ccgggggggg tgtgggggat acccaaatgt aaccgaaaaa tttgaaaacc 2400
ccaaagcccc cgccccttc cttttctccc cttcctttcc ccaaatttcc cgggtttccc 2460
ccgaaaaacc aaaaaacggg ggccc 2485

<210> 10
<211> 601
<212> PRT
<213> Glycine max

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20 25 30

His Pro Phe Ser Gln Ser Gln Ser Thr Lys Tyr Arg Lys Ser Lys His
35 40 45

His His Thr Pro Arg Val Thr Cys Asn Ser Gly Asn Gln Asn Lys Gly
50 55 60

Glu Lys Pro Asp Ile His Ile Glu Gln Arg Arg Asn Ile Leu Leu Gly
65 70 75 80

Leu Gly Gly Leu Cys Gly Ala Ala Thr Leu Asn Asn Asn Pro Phe Ala
85 90 95

Phe Ala Ala Pro Ile Ser Pro Pro Asp Leu Thr Thr Cys Gly Pro Pro
100 105 110

Asp Leu Pro Glu Gly Ala Glu Pro Thr Asn Cys Cys Pro Pro Phe Ser
115 120 125

Ser Thr Ile Ile Asp Phe Lys Phe Pro Pro Ser Asn Lys Pro Leu Arg
130 135 140

Val Arg Pro Ala Ala His Leu Val Asp Lys Asn Tyr Leu Ala Lys Tyr
145 150 155 160

Lys Lys Ala Ile Asp Leu Met Lys Lys Leu Pro Ala Asn Asp Pro Arg
165 170 175

Asn Phe Met Gln Gln Ala Asn Val His Cys Ala Tyr Cys Thr Gly Ser
180 185 190

Tyr Asp Gln Val Gly Phe Pro Gly Leu Glu Leu Gln Val His Ser Ser
195 200 205

Trp Leu Phe Phe Pro Tyr His Arg Trp Phe Leu Tyr Phe Tyr Glu Arg
210 215 220

Ile Leu Gly Ser Leu Ile Asn Asp Pro Thr Phe Ala Leu Pro Phe Trp
225 230 235 240

```
Asn Trp Asp Ala Pro Lys Gly Met Gln Leu Pro Ser Ile Tyr Ala Asp
                245                 250                 255

Pro Lys Ser Pro Leu Tyr Asp Pro Leu Arg Asn Ala Asn His Gln Pro
            260                 265                 270

Pro Thr Leu Val Asp Phe Asp Phe Asn Leu Asp Asn Pro Ile Ser Asn
        275                 280                 285

Gly Arg Ile Ser Thr Asn Leu Thr Ile Met Tyr Arg Gln Leu Val Ser
    290                 295                 300

Asn Gly Lys Thr Pro Thr Leu Phe Leu Gly Asn Pro Tyr Arg Ala Gly
305                 310                 315                 320

Asp Ala Pro Asp Pro Gly Gly Gly Ser Val Glu Gly Val Pro His Gly
                325                 330                 335

Pro Val His Leu Trp Thr Gly Asp Ile Asn Gln Pro Asn Ile Glu Asn
            340                 345                 350

Met Gly Asp Phe Tyr Ser Ala Ala Arg Asp Pro Ile Phe Tyr Ser His
        355                 360                 365

His Ser Asn Val Asp Arg Met Trp Ser Ile Trp Lys Thr Leu Gly Gly
    370                 375                 380

Lys Arg Arg Asp Phe Thr Asp Ser Asp Trp Leu Glu Ser Gly Leu Leu
385                 390                 395                 400

Phe Tyr Asp Glu Asn Lys Asn Leu Val Arg Val Lys Val Lys Asp Cys
                405                 410                 415

Leu Asp Thr Arg Lys Leu Gly Tyr Val Tyr Gln Asp Val Glu Ile Pro
            420                 425                 430

Trp Leu Lys Ser Lys Pro Ser Pro Arg Arg Ser Arg Val Gln Lys Val
        435                 440                 445

Ala Leu Gly Pro His Phe Asn Thr Gly Val Ala Arg Ala Ala Glu Thr
    450                 455                 460

Ser Arg Asn Val Gln Phe Pro Leu Val Leu Asp Ser Val Val Ser Ile
465                 470                 475                 480

Val Val Lys Arg Pro Lys Lys Ser Arg Ser Lys Lys Glu Lys Glu Glu
                485                 490                 495

Glu Glu Glu Val Leu Val Ile Glu Gly Val Glu Tyr Asp Ser Asn Ile
            500                 505                 510

Pro Val Lys Phe Asp Val Leu Ile Asn Asp Glu Asp Asp Lys Gln Ile
        515                 520                 525

Gln Pro Glu Asp Ser Glu Tyr Ala Gly Ser Phe Val Thr Val Pro His
    530                 535                 540

Ser His Lys His Lys Asn Lys Lys Ile Ile Thr Cys Leu Arg Leu Gly
545                 550                 555                 560
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Leu Thr Asp Leu Leu Glu Glu Leu Glu Ala Glu Asp Asp Asp Ser Val
                565                 570                 575

Val Val Thr Leu Val Pro Arg Tyr Gly Lys Gly Arg Val Gln Ile Gly
            580                 585                 590

Gly Ile Lys Ile Asp Leu Val Ala Asp
        595                 600
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<210> 11
<211> 450
<212> DNA
<213> Triticum aestivum

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<222> (20)
<223> n = a, c, g or t

<220>
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<222> (357)
<223> n = a, c, g or t

<220>
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<222> (389)
<223> n = a, c, g or t

<220>
<221> unsure
<222> (412)
<223> n = a, c, g or t

<220>
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<222> (444)
<223> n = a, c, g or t

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cgaggcagac gcggcgcctg acgtgcaagg caaccggcgg ccgcgtcgac cgccgcgacg 180
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<210> 12
<211> 166
<212> PRT
<213> Triticum aestivum

<220>
<221> UNSURE
<222> (163)
<223> Xaa = any amino acid

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Met Glu Ile Ser Thr Ser Val Ala Arg Cys Thr Arg Met Pro Cys Ser
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Leu Gln Ala Leu Val Pro Thr Lys Ala Arg Gln Thr Arg Arg Leu Thr
20 25 30

Cys Lys Ala Thr Gly Gly Arg Val Asp Arg Arg Asp Val Leu Leu Gly
35 40 45

Leu Gly Ser Ala Ala Ala Ala Gly Leu Gly Ala Gln Arg Gly Arg Gly
50 55 60

Ala Ile Ala Ala Pro Ile Gln Ala Pro Asp Leu Gly Asn Cys Asn Pro
65 70 75 80

Pro Asp Leu Pro Asn Thr Ala Pro Asp Thr Asn Cys Cys Pro Thr Ser
85 90 95

Gly Thr Gly Ile Ile Asp Phe Val Leu Pro Pro Ala Pro Arg Ala Pro
100 105 110

Leu Arg Val Arg Pro Ala Ala His Leu Ala Asp Ala Glu Tyr Leu Ala
115 120 125

Lys Tyr Glu Arg Ala Val Ala Leu Met Lys Gln Leu Pro Ala Asp Asp
130 135 140

Pro Arg Ser Ser Lys Gln Gln Trp Arg Val His Cys Ala Tyr Cys Glu
145 150 155 160

Arg Pro Xaa Arg Gln Val
165

<210> 13
<211> 1993
<212> DNA
<213> Triticum aestivum

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actggcttga caccgccttc ctcttctacg acgaggaggc ccgccccgtg cgcgtccgcg 1200

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tcccggcgac gctgagggag accgtgcggg tgacggtgac aaggccccag gtgtcgagga 1380
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ccgtgtggtg tatatctaaa caagtcgctc atgagcgatc gttgcgtgct ttacgtcacg 1800
tatgtctagc gtatattgcg ccgtatgtta cgtgcatcta ctgtgcttat attgcagcgt 1860
atgtctagcg tattctaata agaacaattg gaacggtgca ctttattgtc cttacttcat 1920
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<210> 14
<211> 557
<212> PRT
<213> Triticum aestivum

<400> 14

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Met Glu Ile Ser Thr Ser Val Ala Arg Cys Thr Arg Met Pro Cys Ser
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Leu Gln Ala Leu Val Pro Thr Lys Ala Arg Gln Thr Arg Arg Leu Thr
             20                  25                  30

Cys Lys Ala Thr Gly Gly Arg Val Asp Arg Arg Asp Val Leu Leu Gly
         35                  40                  45

Leu Gly Ser Ala Ala Ala Ala Gly Leu Gly Ala Gln Arg Ala Arg Gly
     50                  55                  60

Ala Ile Ala Ala Pro Ile Gln Ala Pro Asp Leu Gly Asn Cys Asn Pro
 65                  70                  75                  80

Pro Asp Leu Pro Asn Thr Ala Pro Asp Thr Asn Cys Cys Pro Thr Ser
                 85                  90                  95

Gly Thr Gly Ile Ile Asp Phe Val Leu Pro Pro Ala Ser Ser Ala Pro
            100                 105                 110

Leu Arg Val Arg Pro Ala Ala His Leu Ala Asp Ala Glu Tyr Leu Ala
        115                 120                 125

Lys Tyr Glu Arg Ala Val Ala Leu Met Lys Gln Leu Pro Ala Asp Asp
    130                 135                 140

Pro Arg Ser Phe Glu Gln Gln Trp Arg Val His Cys Ala Tyr Cys Asp
145                 150                 155                 160

Gly Ala Tyr Asp Gln Val Gly Phe Pro Asp Leu Glu Ile Gln Val His
                165                 170                 175

Asn Cys Trp Leu Phe Phe Pro Trp His Arg Phe Tyr Leu Tyr Phe His
            180                 185                 190

Glu Arg Ile Leu Gly Lys Leu Ile Gly Asp Asp Thr Phe Ala Leu Pro
        195                 200                 205
```

```
Phe Trp Asn Trp Asp Ala Pro Asp Gly Met Thr Leu Pro Ala Ile Tyr
    210                 215                 220

Ala Asn Arg Ser Ser Pro Leu Tyr Asn Glu Arg Arg Asn Pro Ala His
225                 230                 235                 240

Gln Pro Pro Phe Pro Val Asp Leu Asp Phe Asn Glu Ile Asp Val Ile
                245                 250                 255

Ile Pro Thr Asp Glu Gln Ile Asp Gln Asn Leu Asn Ile Met Tyr Arg
            260                 265                 270

Gln Met Val Ser Gly Ala Lys Lys Thr Arg Leu Phe Met Gly Gln Pro
        275                 280                 285

Tyr Arg Ala Gly Asp Gln Pro Asp Pro Gly Ala Gly Ser Val Glu Asn
    290                 295                 300

Val Pro His Gly Thr Met His Thr Trp Thr Gly Asp Pro Ala Gln Pro
305                 310                 315                 320

Asn Asn Glu Asp Met Gly Asn Phe Tyr Ser Ala Ala Arg Asp Pro Ile
                325                 330                 335

Phe Phe Ala His His Gly Asn Ile Asp Arg Leu Trp His Val Trp Arg
            340                 345                 350

Gly Leu Arg Pro Gly Asn Ala Asp Phe Thr Asp Thr Asp Trp Leu Asp
        355                 360                 365

Thr Ala Phe Leu Phe Tyr Asp Glu Glu Ala Arg Pro Val Arg Val Arg
    370                 375                 380

Val Arg Asp Cys Leu Asp Pro Ala Ala Met Gly Tyr Ala Tyr Gln Asp
385                 390                 395                 400

Val Gly Leu Pro Trp Leu Lys Ala Lys Pro Ala Lys Arg Ser Arg Arg
                405                 410                 415

Thr Pro Ala Pro Ala Ala Gly Ala Leu Pro Ala Thr Leu Arg Glu Thr
            420                 425                 430

Val Arg Val Thr Val Thr Arg Pro Gln Val Ser Arg Ser Asp Lys Glu
        435                 440                 445

Lys Glu Glu Ala Glu Glu Val Leu Ile Val Glu Gly Ile Gln Val Ala
    450                 455                 460

Asp His Phe Lys Phe Val Lys Phe Asp Val Leu Val Asn Ala Pro Glu
465                 470                 475                 480

Ser Gly Gly Asp Ala Ala Ser Gly Tyr Cys Ala Gly Ser Val Ala Met
                485                 490                 495

Thr Pro His Met Val Arg Thr Asn Lys Lys Lys Gly Ser Val Lys Thr
            500                 505                 510

Val Ala Arg Phe Gly Val Cys Asp Leu Met Asp Asn Ile Gly Ala Asp
        515                 520                 525
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Gly Asp Lys Thr Val Val Val Ser Leu Val Pro Arg Cys Gly Gly Glu
530 535 540

Leu Val Thr Ile Gly Gly Val Ser Ile Gly Tyr Thr Lys
545 550 555

<210> 15
<211> 852
<212> DNA
<213> Glycine max

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<223> n = a, c, g or t

<220>
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<221> unsure
<222> (841)
<223> n = a, c, g or t

<220>
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<222> (848)
<223> n = a, c, g or t

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cttcttccct ttccatcgtt ggtatcttta tttctatgaa aggatcttgg ggagcttgat 180
caatgatcca acctttgccc ttccattttg gaactgggat gctcctaagg gcatgcaact 240
tccttccatt tacgcagacc ctaaatcacc cctttatgac actctccgca atgccaatca 300
tcaaccccca acactcgtag acctcgactt caatctcgag gatcctattt ccaatggcaa 360
aatttccaac aacctcacca taatgtatan gcaagttgtg tctaacggga agactcctac 420
attgttcctt ggaaatcctt accgtgctgg ggatgagcct gacccgggtt ttggatcagt 480
agagaatgtt ccacatggcc ctgttcatct ttggnccggt gatatcaacc aacctaacat 540
tgngaacatg ggaactttct attcagctgc aggagacccc atttttatt ctcatcattc 600
agacattgat aagatgtggt ccatatggaa aacactttgt gggaaaagaa gggatttac 660
tgattcantt gggtaaaatc tgcgttctct tctacgatga taacaagaac cttgtgcntn 720
tnaaggcaag gatctcntga cactanaaac taggtatgtt tacaagattt gacatccatg 780
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<210> 16
<211> 221
<212> PRT
<213> Glycine max

<220>
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<222> (130)
<223> Xaa = any amino acid

<220>
<221> UNSURE
<222> (172)
<223> Xaa = any amino acid

<220>
<221> UNSURE
<222> (181)
<223> Xaa = any amino acid

<400> 16

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Pro Ser Asp Asp Pro Arg Asn Phe Thr Gln Gln Ala Asn Val His Cys
  1               5                  10                  15

Ala Tyr Cys Asp Gly Ala Tyr His Gln Val Gly Phe Pro Asp Leu Asp
             20                  25                  30

Leu Gln Val His Asn Ser Trp Leu Phe Phe Pro Phe His Arg Trp Tyr
         35                  40                  45

Leu Tyr Phe Tyr Glu Arg Ile Leu Gly Ser Leu Ile Asn Asp Pro Thr
     50                  55                  60

Phe Ala Leu Pro Phe Trp Asn Trp Asp Ala Pro Lys Gly Met Gln Leu
 65                  70                  75                  80

Pro Ser Ile Tyr Ala Asp Pro Lys Ser Pro Leu Tyr Asp Thr Leu Arg
                85                  90                  95

Asn Ala Asn His Gln Pro Pro Thr Leu Val Asp Leu Asp Phe Asn Leu
            100                 105                 110

Glu Asp Pro Ile Ser Asn Gly Lys Ile Ser Asn Asn Leu Thr Ile Met
        115                 120                 125

Tyr Xaa Gln Val Val Ser Asn Gly Lys Thr Pro Thr Leu Phe Leu Gly
    130                 135                 140

Asn Pro Tyr Arg Ala Gly Asp Glu Pro Asp Pro Gly Phe Gly Ser Val
145                 150                 155                 160

Glu Asn Val Pro His Gly Pro Val His Leu Trp Xaa Gly Asp Ile Asn
                165                 170                 175

Gln Pro Asn Ile Xaa Asn Met Gly Thr Phe Tyr Ser Ala Ala Gly Asp
            180                 185                 190

Pro Ile Phe Tyr Ser His His Ser Asp Ile Asp Lys Met Trp Ser Ile
        195                 200                 205

Trp Lys Thr Leu Cys Gly Lys Arg Arg Asp Phe Thr Asp
    210                 215                 220
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<210> 17
<211> 522
<212> DNA
<213> Glycine max

<400> 17

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catcatattc ctagaatcac atgcagtgga aaccaaaaca atccaacacc aaaccctaat 180
tcccagggag aacctccaca tattgtagga cataggagga acgttctact tggcctagga 240
gggctttgtg gtgctgttac tcttaacaac aacaaccctt ttgcctttgc agctccaata 300
tctcctcctg acctaaacac gtgcggtcca ccagacctac ccgcaggtgt aaaacccacc 360
aattgttgcc ccccatcttc caaaatcata gatttcaagt tctctccctc taaccaaccc 420
ttgagggtaa gaccagccgc acatttggtc aacgatgagt atctagccaa atacaaaaaa 480
agccttgacc tcatgaaaaa actccccctct gatgaccggg tt                   522
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<210> 18
<211> 174

<212> PRT
<213> Glycine max

<400> 18
Ile Ser Pro Leu Ser Phe Val Pro Thr Val Asn Asn Val Ser Ser Asn
1 5 10 15

Ser Ile Ala Pro Pro Ser Pro Leu His Pro Phe Ser Arg Phe Gln Ser
20 25 30

Ile Lys Asn Arg Lys Pro Lys Pro His His Ile Pro Arg Ile Thr Cys
35 40 45

Ser Gly Asn Gln Asn Asn Pro Thr Pro Asn Pro Asn Ser Gln Gly Glu
50 55 60

Pro Pro His Ile Val Gly His Arg Arg Asn Val Leu Leu Gly Leu Gly
65 70 75 80

Gly Leu Cys Gly Ala Val Thr Leu Asn Asn Asn Asn Pro Phe Ala Phe
85 90 95

Ala Ala Pro Ile Ser Pro Pro Asp Leu Asn Thr Cys Gly Pro Pro Asp
100 105 110

Leu Pro Ala Gly Val Lys Pro Thr Asn Cys Cys Pro Pro Ser Ser Lys
115 120 125

Ile Ile Asp Phe Lys Phe Ser Pro Ser Asn Gln Pro Leu Arg Val Arg
130 135 140

Pro Ala Ala His Leu Val Asn Asp Glu Tyr Leu Ala Lys Tyr Lys Lys
145 150 155 160

Ser Leu Asp Leu Met Lys Lys Leu Pro Ser Asp Asp Arg Val
165 170

<210> 19
<211> 1989
<212> DNA
<213> Glycine max

<400> 19
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aaaaccccat catattccta gaatcacatg cagtggaaac caaaacaatc caacaccaaa 180
ccctaattcc cagggagaac ctccacatat tgtaggacat aggaggaacg ttctacttgg 240
cctaggaggg ctttgtggtg ctgttactct taacaacaac aacccttttg cctttgcagc 300
tccaatatct cctcctgacc taaacacgtg cggtccacca gacctacccg caggtgtaaa 360
acccaccaat tgttgccccc catcttccaa aatcatagat ttcaagttct ctccctctaa 420
ccaacccttg agggtaagac cagccgcaca tttggtcaac gatgagtatc tagccaaata 480
caaaaaagcc cttgacctca tgaaaaaact cccctctgat gacccgcgta atttcaccca 540
acaagccaac gttcattgtg cttattgtga tggtgcatat caccaagttg ggttccctga 600
cctcgatctc caagtccaca actcctggct cttcttccct ttccatcgtt ggtatcttta 660
tttctatgaa aggatcttgg ggagcttgat caatgatcca acctttgccc ttccattttg 720
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cctttatgac actctccgca atgccaatca tcaaccccca acactcgtag acctcgactt 840
caatctcgag gatcctattt ccaatggcaa aatttccaac aacctcacca taatgtatag 900
gcaagttgtg tctaacggga agactcctac attgttcctt ggaaatcctt accgtgctgg 960
ggatgagcct gacccgggtt ttggatcagt agagaatgtt ccacatggcc ctgttcatct 1020

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gcgtaggtca agggttcaga aggtagcatt agcacaaaat tttggtgttg gtgcagcaca 1380
tgctgctgag acttcaagga atgtgaagtt cccactagtg ttggattcag ttgtgagcac 1440
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tttggtgatt gaagggattg agtttgagag aaacacacct gtgaaatttg atgtgtttat 1560
caatgatgaa gatgataagc agattcgacc agataataca gaatttgcag gaagctttgt 1620
gagtgtgcct cattcacata tgcacaaaaa caaggacatc attacttgtt tgaggctggg 1680
acttacggat ttgttggaag aattggaagc ggaagatgat gacagtgtta gggtgacgct 1740
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ggattgaaaa ttatctatat gcttcaacta cttatatatg tgtgtgtggt aatacatata 1860
tggttactag tttccaataa agtgtgtaac tcataaagag atattatgta tttcctatca 1920
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aaaaaaaaa                                                        1989
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<210> 20
<211> 599
<212> PRT
<213> Glycine max

<400> 20

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Ile Ser Pro Leu Ser Phe Val Pro Thr Val Asn Asn Val Ser Ser Asn
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Ser Ile Ala Pro Pro Ser Pro Leu His Pro Phe Ser Arg Phe Gln Ser
             20                  25                  30

Ile Lys Asn Arg Lys Pro Lys Pro His His Ile Pro Arg Ile Thr Cys
         35                  40                  45

Ser Gly Asn Gln Asn Asn Pro Thr Pro Asn Pro Asn Ser Gln Gly Glu
     50                  55                  60

Pro Pro His Ile Val Gly His Arg Arg Asn Val Leu Leu Gly Leu Gly
 65                  70                  75                  80

Gly Leu Cys Gly Ala Val Thr Leu Asn Asn Asn Asn Pro Phe Ala Phe
                 85                  90                  95

Ala Ala Pro Ile Ser Pro Pro Asp Leu Asn Thr Cys Gly Pro Pro Asp
            100                 105                 110

Leu Pro Ala Gly Val Lys Pro Thr Asn Cys Cys Pro Pro Ser Ser Lys
        115                 120                 125

Ile Ile Asp Phe Lys Phe Ser Pro Ser Asn Gln Pro Leu Arg Val Arg
    130                 135                 140

Pro Ala Ala His Leu Val Asn Asp Glu Tyr Leu Ala Lys Tyr Lys Lys
145                 150                 155                 160

Ala Leu Asp Leu Met Lys Lys Leu Pro Ser Asp Asp Pro Arg Asn Phe
                165                 170                 175

Thr Gln Gln Ala Asn Val His Cys Ala Tyr Cys Asp Gly Ala Tyr His
            180                 185                 190
```

```
Gln Val Gly Phe Pro Asp Leu Asp Leu Gln Val His Asn Ser Trp Leu
        195                 200                 205

Phe Phe Pro Phe His Arg Trp Tyr Leu Tyr Phe Tyr Glu Arg Ile Leu
    210                 215                 220

Gly Ser Leu Ile Asn Asp Pro Thr Phe Ala Leu Pro Phe Trp Asn Trp
225                 230                 235                 240

Asp Ala Pro Lys Gly Met Gln Leu Pro Ser Ile Tyr Ala Asp Pro Lys
                245                 250                 255

Ser Pro Leu Tyr Asp Thr Leu Arg Asn Ala Asn His Gln Pro Pro Thr
            260                 265                 270

Leu Val Asp Leu Asp Phe Asn Leu Glu Asp Pro Ile Ser Asn Gly Lys
        275                 280                 285

Ile Ser Asn Asn Leu Thr Ile Met Tyr Arg Gln Val Val Ser Asn Gly
    290                 295                 300

Lys Thr Pro Thr Leu Phe Leu Gly Asn Pro Tyr Arg Ala Gly Asp Glu
305                 310                 315                 320

Pro Asp Pro Gly Phe Gly Ser Val Glu Asn Val Pro His Gly Pro Val
                325                 330                 335

His Leu Trp Thr Gly Asp Ile Asn Gln Pro Asn Ile Glu Asn Met Gly
            340                 345                 350

Thr Phe Tyr Ser Ala Ala Arg Asp Pro Ile Phe Tyr Ser His His Ser
        355                 360                 365

Asn Ile Asp Arg Met Trp Ser Ile Trp Lys Thr Leu Gly Gly Lys Arg
    370                 375                 380

Arg Asp Phe Thr Asp Ser Asp Trp Leu Glu Ser Ala Phe Leu Phe Tyr
385                 390                 395                 400

Asp Glu Asn Lys Asn Leu Val Arg Val Lys Val Lys Asp Ser Leu Asp
                405                 410                 415

Thr Arg Lys Leu Gly Tyr Val Tyr Gln Asp Val Asp Ile Pro Trp Leu
            420                 425                 430

Asn Ser Lys Pro Thr Pro Arg Arg Ser Arg Val Gln Lys Val Ala Leu
        435                 440                 445

Ala Gln Asn Phe Gly Val Gly Ala Ala His Ala Ala Glu Thr Ser Arg
    450                 455                 460

Asn Val Lys Phe Pro Leu Val Leu Asp Ser Val Val Ser Thr Met Val
465                 470                 475                 480

Lys Arg Pro Asn Lys Ser Arg Ser Lys Lys Glu Lys Glu Glu Glu Glu
                485                 490                 495

Glu Val Leu Val Ile Glu Gly Ile Glu Phe Glu Arg Asn Thr Pro Val
            500                 505                 510
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```
Lys Phe Asp Val Phe Ile Asn Asp Glu Asp Asp Lys Gln Ile Arg Pro
        515                 520                 525

Asp Asn Thr Glu Phe Ala Gly Ser Phe Val Ser Val Pro His Ser His
    530                 535                 540

Met His Lys Asn Lys Asp Ile Ile Thr Cys Leu Arg Leu Gly Leu Thr
545                 550                 555                 560

Asp Leu Leu Glu Glu Leu Glu Ala Glu Asp Asp Asp Ser Val Arg Val
                565                 570                 575

Thr Leu Val Pro Arg Tyr Gly Lys Gly Arg Val Lys Ile Arg Gly Ile
            580                 585                 590

Lys Ile Glu Leu Leu Ser Asp
        595
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<210> 21
<211> 887
<212> DNA
<213> Glycine max

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<222> (33)
<223> n = a, c, g or t

<220>
<221> unsure
<222> (60)
<223> n = a, c, g or t

<220>
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<222> (618)
<223> n = a, c, g or t

<220>
<221> unsure
<222> (792)
<223> n = a, c, g or t

<220>
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<222> (854)
<223> n = a, c, g or t

<220>
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<222> (865)
<223> n = a, c, g or t

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tctacgatga gaataagaac cttgtgcgag taaaggttaa agattgtctt gacgagagaa 180
aactagggta tgtttaccaa gatgtagaca ttccatggtt aaactctagg cccacaccgc 240
gaaggtctag ggttcaaaag gttgcactag cacaaaattt tggtgttggt gcagcacgtg 300
ctgctgagac ttcaaggaat gtgaagttcc cactagtgtt ggattcagtt gtgagcacaa 360

tggttaaaag gccaaacaag tcgaggagca agaaggagaa ggaagaggag gaagaggttt 420
tggtgattga agggattgag tttgagagaa acacacctgt gaaatttgat gtgtttatca 480
atgatgaaga tgataagcag attcgaccag ataatacaga atttgcagga agctttgtga 540
gtgtgcctca ttcacatatg cacaaaaaca aggacatcat tacttgtttg aggctgggac 600
ttacggattt gttggaanga attggaagcg gaagatgatg acagtgttag ggtgacgctg 660
gttccgagat atgggaaagg gcgtgttaaa atcaagaggc atcaaaatag agcttctttc 720
ggattgaaaa ttatctatat gcttcaacta cttatatatg tgtgtgtggt aatacatata 780
tggttactaa gnttccaata aagtgtgtaa ctcataaaga gatattatgt atttcctatc 840
atatgctgat tcanttaata ctganaaata actaaaagat tatgctt 887

<210> 22
<211> 265
<212> PRT
<213> Glycine max

<220>
<221> UNSURE
<222> (11)
<223> Xaa = any amino acid

<220>
<221> UNSURE
<222> (20)
<223> Xaa = any amino acid

<220>
<221> UNSURE
<222> (263)
<223> Xaa = any amino acid

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His Met Lys Xaa Leu Val Gly Lys Gly Lys Asp Phe Thr Asp Ser Asp
20 25 30

Trp Leu Glu Ser Gly Phe Leu Phe Tyr Asp Glu Asn Lys Asn Leu Val
35 40 45

Arg Val Lys Val Lys Asp Cys Leu Asp Glu Arg Lys Leu Gly Tyr Val
50 55 60

Tyr Gln Asp Val Asp Ile Pro Trp Leu Asn Ser Arg Pro Thr Pro Arg
65 70 75 80

Arg Ser Arg Val Gln Lys Val Ala Leu Ala Gln Asn Phe Gly Val Gly
85 90 95

Ala Ala Arg Ala Ala Glu Thr Ser Arg Asn Val Lys Phe Pro Leu Val
100 105 110

Leu Asp Ser Val Val Ser Thr Met Val Lys Arg Pro Asn Lys Ser Arg
115 120 125

Ser Lys Lys Glu Lys Glu Glu Glu Glu Val Leu Val Ile Glu Gly
130 135 140

Ile Glu Phe Glu Arg Asn Thr Pro Val Lys Phe Asp Val Phe Ile Asn
145 150 155 160

```
Asp Glu Asp Asp Lys Gln Ile Arg Pro Asp Asn Thr Glu Phe Ala Gly
                165                 170                 175

Ser Phe Val Ser Val Pro His Ser His Met His Lys Asn Lys Asp Ile
            180                 185                 190

Ile Thr Cys Leu Arg Leu Gly Leu Thr Asp Leu Leu Glu Glu Leu Glu
        195                 200                 205

Ala Glu Asp Asp Asp Ser Val Arg Val Thr Leu Val Pro Arg Tyr Gly
    210                 215                 220

Lys Gly Arg Val Lys Ile Lys Arg His Gln Asn Arg Ala Ser Phe Gly
225                 230                 235                 240

Leu Lys Ile Ile Tyr Met Leu Gln Leu Leu Ile Tyr Val Cys Val Val
                245                 250                 255

Ile His Ile Trp Leu Leu Xaa Phe Gln
            260                 265
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<210> 23
<211> 510
<212> DNA
<213> Glycine max

<220>
<221> unsure
<222> (478)
<223> n = a, c, g or t

<400> 23

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atcacattcc tagaaccaca tgcagtgaaa accaaaacaa tccaacacca aacccatccg 180
aaggagaact atcacatatt gtaggacata ggaggaatgt tctacttggc ctaggagggc 240
tttgtggtgc agttactctt aacaacaacc cttttgcctt tgcagctcca atatctcctc 300
cagacctaaa cacacatgtg gtccaccaga cacacccgcg ggtgcaaatc ccaccaattt 360
gttgcccccc atcttccaaa aatcatagat ttcaaaggtt ccctccttct aaaccaaccc 420
cttgagggta agaccaagcg ggcacatttg ggtcaaaccg atgaaataat ctaagccnaa 480
aatacaaaaa aaggcccttt gacctcaatg                                  510
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<210> 24
<211> 138
<212> PRT
<213> Glycine max

<400> 24

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Pro Phe Ser Phe Val Ser Val Val Asn Asn Ala Ser Ser Asn Ser Ser
  1               5                  10                  15

Thr Thr Pro Pro Ser Ser Leu His Pro Ile Ser Gln Phe Gln Ser Thr
             20                  25                  30

Lys Asn Arg Lys Pro Lys Arg His His Ile Pro Arg Thr Thr Cys Ser
         35                  40                  45

Glu Asn Gln Asn Asn Pro Thr Pro Asn Pro Ser Glu Gly Glu Leu Ser
     50                  55                  60
```

```
His Ile Val Gly His Arg Arg Asn Val Leu Leu Gly Leu Gly Gly Leu
 65                  70                  75                  80

Cys Gly Ala Val Thr Leu Asn Asn Asn Pro Phe Ala Phe Ala Ala Pro
                85                  90                  95

Ile Ser Pro Pro Asp Leu Asn Thr His Val Val His Gln Thr His Pro
            100                 105                 110

Arg Val Gln Ile Pro Pro Ile Cys Cys Pro Pro Ser Ser Lys Asn His
        115                 120                 125

Arg Phe Gln Arg Phe Pro Pro Ser Lys Pro
    130                 135
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<210> 25
<211> 988
<212> DNA
<213> Glycine max

<220>
<221> unsure
<222> (962)
<223> n = a, c, g or t

<220>
<221> unsure
<222> (970)..(971)
<223> n = a, c, g or t

<400> 25
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ccatcatcat attcctagag tgacatgcag tgacaaccaa aaaccaaaca catctggaga 180
actagtactc ccacatagga ggaacattct acttggccta ggagggcttt gtggtgctgc 240
tgctactctt aacaacatcc cttttgccaa tgctgcccca atacttggtc cagacctaac 300
cacatgtgtt caagcagaac tacccgaagg tgtagaaccc accaattgtt gtcccccaat 360
ttccacaaac atcatagatt tcaagttccc tccctccaac caacccttgc gtgtacgatc 420
cgctgctcat ctggtcaaca aagactatct agctaaatac gagaaagccg ttaacctgat 480
gaaaaatctc ccgtcagatg atccacgtag tttcgcgcaa caagccaaag ttcattgtgc 540
ttattgcgac ggtggatatc accaactagg cttccctgac cttgatctcg aagtgcactt 600
ctcttggctc ttctttcctt accacagatg gtatctctat ttccatgaaa ggatattggc 660
gagcttgatc aatgatccaa cctttgctct tccattttgg aactgggatg ctcctggggg 720
catgcaactt ccttccatgt acgcagatcc caaatcaccc ctttatgatt ctctacgcaa 780
tgccaaccat caaccaccaa cacttgtaaa ccttgacttt actatcgagg atcctaatgc 840
agaggcaaat atctccacca acctcaccac aatgtatagg caagcttgtg tctaacgcaa 900
agactccaac attgttcttc ggaaatcctt atcgtgctgg ggatcagcta accctggtgg 960
gnggtccgtn nagagcactc cacatggg                                    988
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<210> 26
<211> 274
<212> PRT
<213> Glycine max

<400> 26
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Ser Pro Ile Ser Phe Val Ser Ala Ile Asn Asn Val Ser Ser Asn Ser
  1               5                  10                  15

Ser Asn Ser Pro Ser Ser Leu His His Pro Phe Ser Gln Ile Gln Ser
```

```
            20                  25                  30

Ala Lys Tyr Arg Lys Pro Lys Arg His His His Ile Pro Arg Val Thr
         35                  40                  45

Cys Ser Asp Asn Gln Lys Pro Asn Thr Ser Gly Glu Leu Val Leu Pro
     50                  55                  60

His Arg Arg Asn Ile Leu Leu Gly Leu Gly Gly Leu Cys Gly Ala Ala
 65                  70                  75                  80

Ala Thr Leu Asn Asn Ile Pro Phe Ala Asn Ala Ala Pro Ile Leu Gly
                85                  90                  95

Pro Asp Leu Thr Thr Cys Val Gln Ala Glu Leu Pro Glu Gly Val Glu
            100                 105                 110

Pro Thr Asn Cys Cys Pro Pro Ile Ser Thr Asn Ile Ile Asp Phe Lys
        115                 120                 125

Phe Pro Pro Ser Asn Gln Pro Leu Arg Val Arg Ser Ala Ala His Leu
    130                 135                 140

Val Asn Lys Asp Tyr Leu Ala Lys Tyr Glu Lys Ala Val Asn Leu Met
145                 150                 155                 160

Lys Asn Leu Pro Ser Asp Asp Pro Arg Ser Phe Ala Gln Gln Ala Lys
                165                 170                 175

Val His Cys Ala Tyr Cys Asp Gly Gly Tyr His Gln Leu Gly Phe Pro
            180                 185                 190

Asp Leu Asp Leu Glu Val His Phe Ser Trp Leu Phe Phe Pro Tyr His
        195                 200                 205

Arg Trp Tyr Leu Tyr Phe His Glu Arg Ile Leu Ala Ser Leu Ile Asn
    210                 215                 220

Asp Pro Thr Phe Ala Leu Pro Phe Trp Asn Trp Asp Ala Pro Gly Gly
225                 230                 235                 240

Met Gln Leu Pro Ser Met Tyr Ala Asp Pro Lys Ser Pro Leu Tyr Asp
                245                 250                 255

Ser Leu Arg Asn Ala Asn His Gln Pro Pro Thr Leu Val Asn Leu Asp
            260                 265                 270

Phe Thr
```

<210> 27
<211> 2044
<212> DNA
<213> Glycine max

<400> 27
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caaaacgcca tcatcatatt cctagagtga catgcagtga caaccaaaaa ccaaacacat 180
ctggagaact agtactccca cataggagga acattctact tggcctagga gggctttgtg 240

```
gtgctgctgc tactcttaac aacatccctt ttgccaatgc tgccccaata cttggtccag  300
acctaaccac atgtgttcaa gcagaactac ccgaaggtgt agaacccacc aattgttgtc  360
ccccaatttc cacaaacatc atagatttca agttccctcc ctccaaccaa cccttgcgtg  420
tacgatccgc tgctcatctg gtcaacaaag actatctagc taaatacgag aaagccgtta  480
acctgatgaa aaatctcccg tcagatgatc cacgtagttt cgcgcaacaa gccaaagttc  540
attgtgctta ttgcgacggt ggatatcacc aactaggctt ccctgacctt gatctcgaag  600
tgcacttctc ttggctcttc tttccttacc acagatggta tctctatttc catgaaagga  660
tattggcgag cttgatcaat gatccaacct ttgctcttcc attttggaac tgggatgctc  720
ctgggggcat gcaacttcct tccatgtacg cagatcccaa atcacccctt tatgattctc  780
tacgcaatgc caaccatcaa ccaccaacac ttgtaaacct tgactttact atcgaggatc  840
ctaatgcaga ggcaaatatc tccaccaacc tcaccacaat gtataggcag cttgtgtcta  900
acgcaaagac tccaacattg ttcttcggaa atccttatcg tgctggggat cagcctaacc  960
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tctattgcca ccattccaat gttgatagga tgtggtccat atggaaaaca cttggtggga 1140
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cttcaaggaa tgtgaagttc ccattggtgt tggattcagt tgtgagtaca gtggtgaaga 1440
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aagggattga gtttgagagc agcacaggtg tgaagtttga tgtgtttatt aatgatgaag 1560
atgataagtt ggtcaagcca gataatacgg agtttgcagg aagctttgtg agtgtgcctc 1620
attcgcatga gcatcacaaa aacaacaaga agattgttac ttgtttgagg ttgggactaa 1680
cggatttgtt ggaagaattg ggagcagaag atgatgatag tgttctagta acattggttc 1740
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gaaattaaat tgtttatata cttcaaatgt gtgtttgtgc tgtaggtagt aatgcacgca 1860
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aaaa                                                              2044
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<210> 28
<211> 599
<212> PRT
<213> Glycine max

<400> 28

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Thr Ser Ser Pro Ile Ser Phe Val Ser Ala Ile Asn Asn Val Ser Ser
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Asn Ser Ser Asn Ser Pro Ser Ser Leu His His Pro Phe Ser Gln Ile
             20                  25                  30

Gln Ser Ala Lys Tyr Arg Lys Pro Lys Arg His His His Ile Pro Arg
         35                  40                  45

Val Thr Cys Ser Asp Asn Gln Lys Pro Asn Thr Ser Gly Glu Leu Val
     50                  55                  60

Leu Pro His Arg Arg Asn Ile Leu Leu Gly Leu Gly Gly Leu Cys Gly
 65                  70                  75                  80

Ala Ala Ala Thr Leu Asn Asn Ile Pro Phe Ala Asn Ala Ala Pro Ile
                 85                  90                  95

Leu Gly Pro Asp Leu Thr Thr Cys Val Gln Ala Glu Leu Pro Glu Gly
            100                 105                 110

Val Glu Pro Thr Asn Cys Cys Pro Pro Ile Ser Thr Asn Ile Ile Asp
```

```
        115                 120                 125

Phe Lys Phe Pro Pro Ser Asn Gln Pro Leu Arg Val Arg Ser Ala Ala
    130                 135                 140

His Leu Val Asn Lys Asp Tyr Leu Ala Lys Tyr Glu Lys Ala Val Asn
145                 150                 155                 160

Leu Met Lys Asn Leu Pro Ser Asp Asp Pro Arg Ser Phe Ala Gln Gln
                165                 170                 175

Ala Lys Val His Cys Ala Tyr Cys Asp Gly Gly Tyr His Gln Leu Gly
            180                 185                 190

Phe Pro Asp Leu Asp Leu Glu Val His Phe Ser Trp Leu Phe Phe Pro
        195                 200                 205

Tyr His Arg Trp Tyr Leu Tyr Phe His Glu Arg Ile Leu Ala Ser Leu
    210                 215                 220

Ile Asn Asp Pro Thr Phe Ala Leu Pro Phe Trp Asn Trp Asp Ala Pro
225                 230                 235                 240

Gly Gly Met Gln Leu Pro Ser Met Tyr Ala Asp Pro Lys Ser Pro Leu
                245                 250                 255

Tyr Asp Ser Leu Arg Asn Ala Asn His Gln Pro Pro Thr Leu Val Asn
            260                 265                 270

Leu Asp Phe Thr Ile Glu Asp Pro Asn Ala Glu Ala Asn Ile Ser Thr
        275                 280                 285

Asn Leu Thr Thr Met Tyr Arg Gln Leu Val Ser Asn Ala Lys Thr Pro
    290                 295                 300

Thr Leu Phe Phe Gly Asn Pro Tyr Arg Ala Gly Asp Gln Pro Asn Pro
305                 310                 315                 320

Gly Gly Gly Ser Val Glu Ser Thr Pro His Gly Pro Val His Ala Trp
                325                 330                 335

Thr Gly Asp Ile Asn His Pro Thr Met Glu Asp Met Gly Asn Leu Tyr
            340                 345                 350

Ala Ala Ala Arg Asp Pro Ile Phe Tyr Cys His His Ser Asn Val Asp
        355                 360                 365

Arg Met Trp Ser Ile Trp Lys Thr Leu Gly Gly Lys Arg Arg Asp Leu
    370                 375                 380

Thr Asp Pro Asp Trp Leu Glu Ser Ala Phe Leu Phe Tyr Asp Glu Asn
385                 390                 395                 400

Lys Asn Leu Val Arg Val Lys Thr Lys Asp Cys Leu Asp Thr Arg Lys
                405                 410                 415

Leu Gly Tyr Val Tyr Gln Asp Val Asp Ile Pro Trp Leu Lys Ser Lys
            420                 425                 430

Pro Thr Pro Leu Arg Ser Arg Ala Gln Lys Val Glu Leu Thr Pro Leu
```

```
        435                 440                 445

Phe Gly Gly Val Ala Ala Ala His Ala Ala Glu Thr Ser Arg Asn Val
    450                 455                 460

Lys Phe Pro Leu Val Leu Asp Ser Val Val Ser Thr Val Val Lys Arg
465                 470                 475                 480

Pro Lys Lys Ser Arg Ser Lys Lys Glu Lys Glu Glu Lys Glu Glu Ile
                485                 490                 495

Leu Val Val Glu Gly Ile Glu Phe Glu Ser Ser Thr Gly Val Lys Phe
            500                 505                 510

Asp Val Phe Ile Asn Asp Glu Asp Asp Lys Leu Val Lys Pro Asp Asn
        515                 520                 525

Thr Glu Phe Ala Gly Ser Phe Val Ser Val Pro His Ser His Glu His
    530                 535                 540

His Lys Asn Asn Lys Lys Ile Val Thr Cys Leu Arg Leu Gly Leu Thr
545                 550                 555                 560

Asp Leu Leu Glu Glu Leu Gly Ala Glu Asp Asp Asp Ser Val Leu Val
                565                 570                 575

Thr Leu Val Pro Lys Tyr Gly Lys Gly Arg Val Asn Ile Arg Gly Ile
            580                 585                 590

Lys Ile Asp Phe Val Ser Asp
        595
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<210> 29
<211> 685
<212> DNA
<213> Glycine max

<220>
<221> unsure
<222> (478)
<223> n = a, c, g or t

<220>
<221> unsure
<222> (480)
<223> n = a, c, g or t

<220>
<221> unsure
<222> (555)
<223> n = a, c, g or t

<220>
<221> unsure
<222> (570)
<223> n = a, c, g or t

<220>
<221> unsure
<222> (588)

<223> n = a, c, g or t

<220>
<221> unsure
<222> (590)
<223> n = a, c, g or t

<220>
<221> unsure
<222> (607)
<223> n = a, c, g or t

<220>
<221> unsure
<222> (613)
<223> n = a, c, g or t

<220>
<221> unsure
<222> (618)..(619)
<223> n = a, c, g or t

<220>
<221> unsure
<222> (639)
<223> n = a, c, g or t

<220>
<221> unsure
<222> (644)
<223> n = a, c, g or t

<220>
<221> unsure
<222> (675)
<223> n = a, c, g or t

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ctgcacctct tcccatttcc atttgttctt catcttccac cttcctaact tcccaaatac 120
catgcaaacc caccaaacgt agcaaaccaa aacgccacca cgtttcgaaa gtgacatgca 180
acagtaacca aaacacccca acaccaaacc cagaagaaga aagaccatca tacaacattc 240
taggaaaata tagaagggat gttctccttg gcattggggg cctttacggt gcatctgctc 300
ttagcaacac caacccttta gccatggctg cagctcctat tctagagcct gacctagaac 360
attgttgtat aactgatgat gtaccaccta aaggggtcat cgaggcacaa gtctattgtt 420
gcccaccaag atcttcttcc cctcctatag atttcaagtt gcctaaagga acaccctnan 480
ggttagacca cctgctcaat tcgtcactga tggagtacct agaaaagtag aagttagccc 540
ttaagcgcat ggganagttc catctgatgn tctcgagttc aggaacangn tggtatcaat 600
gggcttntgt ganggggnnt aaacaatagg gtcccaacng agcnaggtta aggtcacttt 660
ctggcggtct ccctncacgt tggac 685

<210> 30
<211> 179
<212> PRT
<213> Glycine max

<220>
<221> UNSURE
<222> (155)..(156)
<223> Xaa = any amino acid

<220>
<221> UNSURE
<222> (172)
<223> Xaa = any amino acid

<400> 30
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1 5 10 15

Ala Pro Leu Pro Ile Ser Ile Cys Ser Ser Ser Ser Thr Phe Leu Thr
20 25 30

Ser Gln Ile Pro Cys Lys Pro Thr Lys Arg Ser Lys Pro Lys Arg His
35 40 45

His Val Ser Lys Val Thr Cys Asn Ser Asn Gln Asn Thr Pro Thr Pro
50 55 60

Asn Pro Glu Glu Glu Arg Pro Ser Tyr Asn Ile Leu Gly Lys Tyr Arg
65 70 75 80

Arg Asp Val Leu Leu Gly Ile Gly Gly Leu Tyr Gly Ala Ser Ala Leu
85 90 95

Ser Asn Thr Asn Pro Leu Ala Met Ala Ala Ala Pro Ile Leu Glu Pro
100 105 110

Asp Leu Glu His Cys Cys Ile Thr Asp Asp Val Pro Pro Lys Gly Val
115 120 125

Ile Glu Ala Gln Val Tyr Cys Cys Pro Pro Arg Ser Ser Ser Pro Pro
130 135 140

Ile Asp Phe Lys Leu Pro Lys Gly Thr Pro Xaa Xaa Leu Asp His Leu
145 150 155 160

Leu Asn Ser Ser Leu Met Glu Tyr Leu Glu Lys Xaa Lys Leu Ala Leu
165 170 175

Lys Arg Met

<210> 31
<211> 1994
<212> DNA
<213> Glycine max

<400> 31
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caaataccat gcaaaccctc caaacgtagc aaaccaaaag gccatcatgt ttccaaagtg 180
tcatgcaaca gtaaccaaaa caccccaaca ccaaacccag aagaagaaaa accatcgtca 240
tacaacattc taggaaaaca taggagggat attctccttg gcattggggg cctttacggt 300
gcttctgctc ttagcaacac caacccttta gccatggctg cagctcctat tctagagcct 360
gacctagaac attgttgtat aactgatgat gtacctaaag gggaaatcga gaaacaagtc 420
tattgttgcc caccaaaatc ttcttccccc cctatagatt tcaagttgcc taaaggaaca 480
ccccttaggg ttagaccacc tgctcaattt gtgaccgatg agtacctaga aaagtataag 540
ttagccctta agcgcatgag agagcttcca tctgatgatc ctcgaagttt caagcaacaa 600
gctgatatcc attgtgctta ttgtgatggt ggctataagc aattagggtt cccagttgag 660

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aactgggaca atcctgatgg tggcatggta ttgccttcca ttttcgcaga tgaagactcc  840
cctctatatg accctcgcag gaatccagac atcacaccaa ctactctcgt agacctaaac  900
tatggcagtg gaaaggaacc aagcgtagaa caaaacctcg gtgtaatgta tacgagtgtt  960
gtctctggtg cgaaacgcgc atcgctcttc catggaaaac catttcttgc tggaaagcag 1020
cctgagctaa gtggagggac cgtagagctt ggtcctcata ctgctgtcca ccgttggacc 1080
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ccaagtggaa aaagaaggga tttcaaaaac cgtgattggt tggaaacctc ctttttcttc 1260
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gagtttgaga aggatgagtg aaaatatgtc actcatttac tactaaacat gcaaatgagt 1920
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aaaaaaaaaa aaaa                                                   1994
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<210> 32
<211> 619
<212> PRT
<213> Glycine max

<400> 32

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Met Ala Tyr Ile Ser Ser Leu Ser Ser Phe Ser Leu Ser Asn Phe Ser
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Ala Pro Leu Pro Ile Ser Ile Cys Ser Ser Ser Ser Ala Phe Leu Thr
             20                  25                  30

Ser Gln Ile Pro Cys Lys Pro Ser Lys Arg Ser Lys Pro Lys Gly His
         35                  40                  45

His Val Ser Lys Val Ser Cys Asn Ser Asn Gln Asn Thr Pro Thr Pro
     50                  55                  60

Asn Pro Glu Glu Glu Lys Pro Ser Ser Tyr Asn Ile Leu Gly Lys His
 65                  70                  75                  80

Arg Arg Asp Ile Leu Leu Gly Ile Gly Gly Leu Tyr Gly Ala Ser Ala
                 85                  90                  95

Leu Ser Asn Thr Asn Pro Leu Ala Met Ala Ala Ala Pro Ile Leu Glu
            100                 105                 110

Pro Asp Leu Glu His Cys Cys Ile Thr Asp Asp Val Pro Lys Gly Glu
        115                 120                 125

Ile Glu Lys Gln Val Tyr Cys Cys Pro Pro Lys Ser Ser Ser Pro Pro
    130                 135                 140

Ile Asp Phe Lys Leu Pro Lys Gly Thr Pro Leu Arg Val Arg Pro Pro
145                 150                 155                 160
```

```
Ala Gln Phe Val Thr Asp Glu Tyr Leu Glu Lys Tyr Lys Leu Ala Leu
                  165                 170                 175

Lys Arg Met Arg Glu Leu Pro Ser Asp Asp Pro Arg Ser Phe Lys Gln
             180                 185                 190

Gln Ala Asp Ile His Cys Ala Tyr Cys Asp Gly Gly Tyr Lys Gln Leu
         195                 200                 205

Gly Phe Pro Val Glu Leu Asp Phe Lys Val His Phe Ser Trp Ile Phe
     210                 215                 220

Phe Pro Phe His Arg Trp Tyr Leu Tyr Phe Tyr Glu Arg Ile Leu Gly
225                 230                 235                 240

Ser Leu Ile Asp Asp Pro Thr Phe Ala Leu Pro Tyr Trp Asn Trp Asp
                  245                 250                 255

Asn Pro Asp Gly Gly Met Val Leu Pro Ser Ile Phe Ala Asp Glu Asp
             260                 265                 270

Ser Pro Leu Tyr Asp Pro Arg Arg Asn Pro Asp Ile Thr Pro Thr Thr
         275                 280                 285

Leu Val Asp Leu Asn Tyr Gly Ser Gly Lys Glu Pro Ser Val Glu Gln
     290                 295                 300

Asn Leu Gly Val Met Tyr Thr Ser Val Val Ser Gly Ala Lys Arg Ala
305                 310                 315                 320

Ser Leu Phe His Gly Lys Pro Phe Leu Ala Gly Lys Gln Pro Glu Leu
                  325                 330                 335

Ser Gly Gly Thr Val Glu Leu Gly Pro His Thr Ala Val His Arg Trp
             340                 345                 350

Thr Gly Asp Pro Arg Gln Pro Asn Lys Glu Asp Met Gly Arg Phe Tyr
         355                 360                 365

Ser Ala Gly Arg Asp Pro Ala Phe Tyr Ser His His Ala Asn Val Asp
     370                 375                 380

Arg Met Trp Asn Ile Trp Lys Thr Ile Pro Ser Gly Lys Arg Arg Asp
385                 390                 395                 400

Phe Lys Asn Arg Asp Trp Leu Glu Thr Ser Phe Phe Phe Tyr Asp Glu
                  405                 410                 415

Asn Lys Thr Leu Val Arg Val Lys Val Lys Asp Ser Leu Asp Thr Asn
             420                 425                 430

Lys Met Gly Tyr Val Tyr Gln Asp Val Ala Ile Pro Trp Leu Glu Lys
         435                 440                 445

Lys Pro Lys Pro Lys Arg Thr Arg Lys Ala Lys Lys Val Ala Phe Ala
     450                 455                 460

Gln Gln Phe Gly Gly Ile Gly Ala Ala Met Ala Ala Glu Thr Gly Pro
465                 470                 475                 480
```

```
Ser Ser Lys Phe Pro Leu Thr Leu Leu Asp Ser Lys Val Thr Leu Leu
                485                 490                 495

Val Lys Arg Pro Lys Gln Leu Arg Ser Lys Arg Asp Lys Glu Glu Glu
            500                 505                 510

Glu Glu Val Leu Val Ile Asp Gly Ile Glu Phe Asp Gly Asp Asp Asp
        515                 520                 525

Val Lys Phe Asp Val Tyr Ile Thr Asp Glu Asp Val Glu Asp Ile Gly
    530                 535                 540

Pro Glu Ser Thr Glu Phe Ala Gly Ser Phe Ser Thr Leu Gly His Ser
545                 550                 555                 560

His Ser Asn Met Asn Met Asp Lys Lys Ile Lys Thr Ser Leu Thr Leu
                565                 570                 575

Gly Ile Thr Asp Leu Leu Glu Asp Leu Asp Ala Glu Asn Asp Asp Ser
            580                 585                 590

Val Leu Val Thr Leu Val Pro Arg Ser Glu Asn Val Thr Ile Thr Ile
        595                 600                 605

Gln Asn Ile Lys Ile Glu Phe Glu Lys Asp Glu
    610                 615
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<210> 33
<211> 2028
<212> DNA
<213> Glycine max

<400> 33

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tgcaatggta accctagaaa taggagggac attctgatcg gccttggagg actctatggt  180
gctacaacaa gtctcacaag taacaacact ggttctgcat ttggtgcttc attgtcgcct  240
ccagatccaa ctaactgcgt tcaaccggac ccagaaaaag acccttttg cccaccaccc  300
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ccagctgctc atttggtcac tgatgattac atagccaagt acgaggaagc cgtgaggcgc  420
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gcctactgcg atggtcgcgg ctatactcaa aagggcttcg ctgactacaa gcttgacgtt  540
cacggctcct ggatattctt tccttggcac cgctggtatc tctatttcta tgagaaaatc  600
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aggaatagcg atcatgtaaa tgctttcatc gacctagact acaagaagga cgattctcct  780
gtgaaacctc ctcaaacaat tttatggccg ccagtggaga aaaagaataa ctcgatcgtc  840
gacaacttga tcgtcaacaa cttgataaaa gtttatacgg cagttgcaag caaaaccaac  900
tcaagcccag actacttcct cgggccagca ttcgaagctg gttctgcacc tcagcaacac  960
tttggatctc tggaatcttt gcacaatact gtccacagct ggaccggtga aagagaaaac 1020
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gaagaagaag aagaaggcgt agaagaggtg ttagtgatag atgttgagta cgatagcact 1500
gatggtgtga ggtttgatgt gttcatcaac gaccaaggcg acaatgagat tggaccccag 1560
gattcagagt ttgcgggaag ctttgtgact ttgcctcact cgccgcatgt caaccataac 1620
```

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aacatcacca aagcttcttt caaattgcca ttaacgtata agttgaaaga cttgggagta 1680
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attatgtgtg tgctactgct agggtttgtt cctccaaggg atactctatc tgtcatttgt 1860
tgtttcttaa ttagtgtgtt gtagttattt tccttggaac ttaatagatc cctttcatct 1920
gtgagggata ctatgttatt gttataataa atgtttgttt tattgttaca tttgtttata 1980
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<210> 34
<211> 597
<212> PRT
<213> Glycine max

<400> 34

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Ala Arg Gly Ser Leu Leu Asn Leu Ser Ala Ser Ile Pro Ile Ser Ser
  1               5                  10                  15

Ser Val Cys Met Phe Pro Pro Ser Lys Lys Pro Ser Lys Ala Thr Lys
             20                  25                  30

Arg Arg His Ala Trp Glu Val Ala Cys Asn Gly Asn Pro Arg Asn Arg
         35                  40                  45

Arg Asp Ile Leu Ile Gly Leu Gly Gly Leu Tyr Gly Ala Thr Thr Ser
     50                  55                  60

Leu Thr Ser Asn Asn Thr Gly Ser Ala Phe Gly Ala Ser Leu Ser Pro
 65                  70                  75                  80

Pro Asp Pro Thr Asn Cys Val Gln Pro Asp Pro Glu Lys Asp Pro Phe
                 85                  90                  95

Cys Pro Pro Pro Pro Phe Lys Asp Tyr Glu Leu Pro Pro His Asp Asp
            100                 105                 110

Lys Thr Leu Pro Leu Arg Ile Arg Pro Ala Ala His Leu Val Thr Asp
        115                 120                 125

Asp Tyr Ile Ala Lys Tyr Glu Glu Ala Val Arg Arg Met Gln Asp Leu
    130                 135                 140

Pro Pro Asp Asp Pro Arg Ser Phe Met Gln Gln Ala Asn Val His Arg
145                 150                 155                 160

Ala Tyr Cys Asp Gly Arg Gly Tyr Thr Gln Lys Gly Phe Ala Asp Tyr
                165                 170                 175

Lys Leu Asp Val His Gly Ser Trp Ile Phe Phe Pro Trp His Arg Trp
            180                 185                 190

Tyr Leu Tyr Phe Tyr Glu Lys Ile Leu Gly Lys Met Ile Gly Asp Pro
        195                 200                 205

Thr Phe Ala Leu Pro Phe Trp Asn Trp Asp Asn Pro Ala Gly Met Arg
    210                 215                 220

Ile Pro Pro Ile Phe Thr Asp Lys Ser Ser Pro Leu Tyr Asp Glu His
225                 230                 235                 240

Arg Asn Ser Asp His Val Asn Ala Phe Ile Asp Leu Asp Tyr Lys Lys
```

```
                245                 250                 255

Asp Asp Ser Pro Val Lys Pro Pro Gln Thr Ile Leu Trp Pro Pro Val
            260                 265                 270

Glu Lys Lys Asn Asn Ser Ile Val Asp Asn Leu Ile Val Asn Asn Leu
        275                 280                 285

Ile Lys Val Tyr Thr Ala Val Ala Ser Lys Thr Asn Ser Ser Pro Asp
    290                 295                 300

Tyr Phe Leu Gly Pro Ala Phe Glu Ala Gly Ser Ala Pro Gln Gln His
305                 310                 315                 320

Phe Gly Ser Leu Glu Ser Leu His Asn Thr Val His Ser Trp Thr Gly
                325                 330                 335

Glu Arg Glu Asn Asn His His Asp Met Gly Leu Leu Ala Thr Ala Ala
            340                 345                 350

Lys Asp Pro Ile Phe Phe Ala His His Ser Asn Val Asp Arg Met Trp
        355                 360                 365

Asn Ile Trp Lys Thr Glu Leu Leu Asp Gly Arg Arg Phe Asp His Lys
    370                 375                 380

Ser Asp Asp Trp Leu Glu Ser Ser Phe Phe Phe Tyr Asp Glu Asn Lys
385                 390                 395                 400

Asn Tyr Val Arg Val Lys Val Lys Asp Cys Leu Asp Ser Lys Lys Met
                405                 410                 415

Gly Tyr Asp Tyr Gln Arg Val Asp Leu Pro Trp Leu Leu Ala Gly Glu
            420                 425                 430

Leu Ile Lys Pro Lys Lys Glu Ile Ile Leu Leu Arg Ser Lys Pro Glu
        435                 440                 445

Ala Ser Thr Phe Lys Thr Leu Gln Leu Pro Leu Pro Leu Glu Ser Ile
    450                 455                 460

Glu Arg Thr Asn Val Lys Arg Pro Lys Pro Arg Ser Arg Asn Glu Asn
465                 470                 475                 480

Glu Glu Glu Glu Glu Gly Val Glu Glu Val Leu Val Ile Asp Val Glu
                485                 490                 495

Tyr Asp Ser Thr Asp Gly Val Arg Phe Asp Val Phe Ile Asn Asp Gln
            500                 505                 510

Gly Asp Asn Glu Ile Gly Pro Gln Asp Ser Glu Phe Ala Gly Ser Phe
        515                 520                 525

Val Thr Leu Pro His Ser Pro His Val Asn His Asn Asn Ile Thr Lys
    530                 535                 540

Ala Ser Phe Lys Leu Pro Leu Thr Tyr Lys Leu Lys Asp Leu Gly Val
545                 550                 555                 560

Thr Lys Asp Asp Asp Ser Ile Ser Val Thr Leu Ala Pro Ile Tyr Gly
```

```
                565                 570                 575

Asp Lys Pro Val Thr Ile Lys Asp Val Arg Ile Lys Arg Val Tyr Pro
            580                 585                 590

Glu Val Asp Asp Glu
        595
```

<210> 35
<211> 2260
<212> DNA
<213> Glycine max

<400> 35

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gtcttgctga tgcccttagt ttccttactc aacaatgatt tctctatctt caccattaaa  180
accatttcat acctagtttc ctttagtgaa aagccaaacc attactctaa tttcagcatt  240
attccataca aagcccaaaa tagtaaacaa aatggccaca tcaccacaaa ctccaatgga  300
agagacaaac cacgtctttg gaggaaagcc ttcattggct tcaaaaatac tcacgagcca  360
tcttcgaata tttctcgagc aatatccctt aatgtaagca agtgttttcc cgttgagtta  420
ccttcttttg caataaccaa ttcccattgt tgtccaccta gaccacctcc ttctaagatc  480
atagatttca aagattttgc ttctccaaac gccacgcttc gagtaagaaa accggctcac  540
atggtagatg aggagtacat agcaaaactt gaaaagggca ttgcactcat gaaagcactc  600
cctgatgatg acccacgtaa tttcatacaa caagcaaagg tccattgtgc ttattgtaac  660
ggtgcctatc acctacccca tccctttcag aacacaaaac tcaacattca caggtcttgg  720
tttttctttc ctttccaccg ttggtacatt tacttcttcg agcgaatctt gggaagcttg  780
ctcggtgacc cgaactttgc cttaccgttt tggaattggg atgctgtaga agggatgcaa  840
atgccaccat atttcgcaaa ccctaactcg tcgctctatc acaaactccg aaaccccaag  900
cacttgccac cgcaagtggt tgacctgaac tatgatccat ttgactttaa tgatgataca  960
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aagccacacc aggaggacat gggaacgttc tacacagctg ctagagatcc cgttttctat 1200
ccgcatcaca cgaactcgga tcgactgtgg gggatatgga aaaaattggg agaaggaaga 1260
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gtcgagctcg tattctctgt ggctggattt tgtccaacta actgaaatat gagatgtcga 2040
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tggatgtggg gaagtactcc tagaagtaga tataaatttg ttgtggtgca tgtctttcaa 2160
cactagtgca tgtaaagaaa atcaaataaa tcaatttgat tttctagaac taattttcat 2220
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<210> 36
<211> 601
<212> PRT
<213> Glycine max

<400> 36

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Met Ser Thr Pro Ser Lys Leu Leu Ser Leu Phe Phe Val Leu Ile Val
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  1               5                  10                  15

Leu Leu Met Pro Leu Val Ser Leu Leu Asn Asn Asp Phe Ser Ile Phe
            20                  25                  30

Thr Ile Lys Thr Ile Ser Tyr Leu Val Ser Phe Ser Glu Lys Pro Asn
        35                  40                  45

His Tyr Ser Asn Phe Ser Ile Ile Pro Tyr Lys Ala Gln Asn Ser Lys
    50                  55                  60

Gln Asn Gly His Ile Thr Thr Asn Ser Asn Gly Arg Asp Lys Pro Arg
65                  70                  75                  80

Leu Trp Arg Lys Ala Phe Ile Gly Phe Lys Asn Thr His Glu Pro Ser
                85                  90                  95

Ser Asn Ile Ser Arg Ala Ile Ser Leu Asn Val Ser Lys Cys Phe Pro
            100                 105                 110

Val Glu Leu Pro Ser Phe Ala Ile Thr Asn Ser His Cys Cys Pro Pro
        115                 120                 125

Arg Pro Pro Pro Ser Lys Ile Ile Asp Phe Lys Asp Phe Ala Ser Pro
    130                 135                 140

Asn Ala Thr Leu Arg Val Arg Lys Pro Ala His Met Val Asp Glu Glu
145                 150                 155                 160

Tyr Ile Ala Lys Leu Glu Lys Gly Ile Ala Leu Met Lys Ala Leu Pro
                165                 170                 175

Asp Asp Asp Pro Arg Asn Phe Ile Gln Gln Ala Lys Val His Cys Ala
            180                 185                 190

Tyr Cys Asn Gly Ala Tyr His Leu Pro His Pro Phe Gln Asn Thr Lys
        195                 200                 205

Leu Asn Ile His Arg Ser Trp Phe Phe Phe Pro Phe His Arg Trp Tyr
    210                 215                 220

Ile Tyr Phe Phe Glu Arg Ile Leu Gly Ser Leu Leu Gly Asp Pro Asn
225                 230                 235                 240

Phe Ala Leu Pro Phe Trp Asn Trp Asp Ala Val Glu Gly Met Gln Met
                245                 250                 255

Pro Pro Tyr Phe Ala Asn Pro Asn Ser Ser Leu Tyr His Lys Leu Arg
            260                 265                 270

Asn Pro Lys His Leu Pro Pro Gln Val Val Asp Leu Asn Tyr Asp Pro
        275                 280                 285

Phe Asp Phe Asn Asp Asp Thr Pro Ser His Gln Gln Val Ser Tyr Asn
    290                 295                 300

Leu Ala Phe Met Tyr Lys Gln Met Val Leu Ala Ser Thr Lys Glu Leu
305                 310                 315                 320

Phe Met Gly Ser Pro Phe Arg Leu Gly Asp Asn Pro Thr Pro Gly Ile
```

```
                325                 330                 335

Gly Ser Ile Glu Ala Ala Pro His Asn Thr Val His Lys Trp Val Gly
            340                 345                 350

Ala Ala Asp Lys Pro His Gln Glu Asp Met Gly Thr Phe Tyr Thr Ala
        355                 360                 365

Ala Arg Asp Pro Val Phe Tyr Pro His His Thr Asn Ser Asp Arg Leu
    370                 375                 380

Trp Gly Ile Trp Lys Lys Leu Gly Glu Gly Arg Lys Asp Tyr Ser Asp
385                 390                 395                 400

Asp Pro Asp Trp Leu Asp Ser Asp Phe Tyr Phe Tyr Asp Glu Asn Ala
                405                 410                 415

Asn Phe Val Arg Val Lys Val Arg Asp Cys Phe Asp Thr Lys Arg Leu
            420                 425                 430

Gly Tyr Val Tyr Glu Asp Val Asp Leu Pro Trp Leu Arg Thr Pro Pro
        435                 440                 445

Thr Ser Arg Lys Ser Lys Leu Leu Arg Glu Ala Lys Lys Gly Ser Leu
    450                 455                 460

Leu Ser Ser Lys Pro Trp Lys Phe Pro Leu Val Leu Asp Ser Ile Thr
465                 470                 475                 480

Ser Ile Val Val Lys Arg Pro Lys Lys Trp Arg Ser Lys Glu Glu Lys
                485                 490                 495

Glu Gln Glu Glu Glu Val Leu Val Ile Glu Gly Ile Glu Phe Gly Ser
            500                 505                 510

Asp Lys Tyr Val Lys Phe Asp Val His Ile Asp Asp Asp Glu Asp Asn
        515                 520                 525

Leu Ser Gly Pro Asp Glu Thr Glu Phe Val Gly Ser Phe Val Asn Val
    530                 535                 540

Gln His Gly His Gly His Asn Val Lys Thr Ser Phe Lys Val Gly Ile
545                 550                 555                 560

Ser Lys Val Leu Glu Ser Val Glu Ala Glu Glu Asp Asp Glu Val Leu
                565                 570                 575

Val Ser Leu Val Pro Lys Val Gly Lys Gly Asp Ala Ile Ile Gly Gly
            580                 585                 590

Ile Lys Ile Glu Phe Ile Pro Lys Tyr
        595                 600
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<210> 37
<211> 1141
<212> DNA
<213> Zea mays

<220>
<221> unsure

<222> (16)
<223> n = a, c, g or t

<220>
<221> unsure
<222> (60)
<223> n = a, c, g or t

<400> 37
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tggactacct caagaaaccc agacgcgaca ccatcccttt cgagccgccg acggacccag 120
ccgcgcgcgc caagtacgac gacgccgttc aaaccaacct gtgcaccata tacctgcagc 180
aagtccgtga cggcaagggc ccccgtgctt tcctcggcga gaagctgtgc agcgaccagg 240
gcacgctgga gcggatggcg cacacgacgg tgcacgtgtg gacggggcgg gcgaacccgg 300
cgacgtgcag cgcggagcag ggcggcgtgg tggggcacga cggcaagccg cactgccagg 360
tggacatggg gttcctgggc acggcggggc gtgacccgct cttctactcg caccacgcga 420
acgtggaccg catgtggcac atctggtcca ctaggctggg cggtaagggc ttcgacgacc 480
cggagtggct ggacaccagc ttcgtgttct acgacgacta ccggagccgc ggctggtgac 540
agatgaagtt ccgcgacgtc ctgaacgcga ccaggctcgg gtacacgtac gacaaggagt 600
cggaggcggc gctgccgtgg ctgaacagca agccgacccg gttctccggc ggcggcaagg 660
cgaaggcgaa ggcggcgccc aaggtggcgt cggagttccc gctgaccctg acggacgagg 720
ccgtggacgt gccggcggtg gcggtcccgg cgcggcaggc cgggaaggac ctggtgctgc 780
tgatcgaggg catcgagtac gacccccaga tcaacaacaa gttcgacgtg gtcatcaacg 840
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gcgccgtgcc cagctccaac gccgccggtg gcacgctggt gggcaagttc acgctcgccc 960
tcgacggcgt gctcgccgac ctcgggctcg ccggcgcgag cgccgtcgac atcgtgctcg 1020
tccctcacac ggagggcgag atcaagctgt acttgccccc gaccatcgag aacgcgtgag 1080
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<210> 38
<211> 358
<212> PRT
<213> Zea mays

<220>
<221> UNSURE
<222> (5)
<223> Xaa = any amino acid

<220>
<221> UNSURE
<222> (20)
<223> Xaa = any amino acid

<220>
<221> UNSURE
<222> (179)
<223> Xaa = any amino acid

<400> 38
Asp Asn Pro Leu Xaa Asp Pro Tyr Arg Asn Met Glu Asn Met Asp Ala
1 5 10 15

Leu Leu Asp Xaa Asp Tyr Leu Lys Lys Pro Arg Arg Asp Thr Ile Pro
20 25 30

Phe Glu Pro Pro Thr Asp Pro Ala Ala Arg Ala Lys Tyr Asp Asp Ala
35 40 45

```
Val Gln Thr Asn Leu Cys Thr Ile Tyr Leu Gln Gln Val Arg Asp Gly
     50                  55                  60

Lys Gly Pro Arg Ala Phe Leu Gly Glu Lys Leu Cys Ser Asp Gln Gly
 65                  70                  75                  80

Thr Leu Glu Arg Met Ala His Thr Thr Val His Val Trp Thr Gly Arg
                 85                  90                  95

Ala Asn Pro Ala Thr Cys Ser Ala Glu Gln Gly Gly Val Val Gly His
            100                 105                 110

Asp Gly Lys Pro His Cys Gln Val Asp Met Gly Phe Leu Gly Thr Ala
        115                 120                 125

Gly Arg Asp Pro Leu Phe Tyr Ser His His Ala Asn Val Asp Arg Met
    130                 135                 140

Trp His Ile Trp Ser Thr Arg Leu Gly Gly Lys Gly Phe Asp Asp Pro
145                 150                 155                 160

Glu Trp Leu Asp Thr Ser Phe Val Phe Tyr Asp Asp Tyr Arg Ser Arg
                165                 170                 175

Gly Trp Xaa Gln Met Lys Phe Arg Asp Val Leu Asn Ala Thr Arg Leu
            180                 185                 190

Gly Tyr Thr Tyr Asp Lys Glu Ser Glu Ala Ala Leu Pro Trp Leu Asn
        195                 200                 205

Ser Lys Pro Thr Arg Phe Ser Gly Gly Gly Lys Ala Lys Ala Lys Ala
    210                 215                 220

Ala Pro Lys Val Ala Ser Glu Phe Pro Leu Thr Leu Thr Asp Glu Ala
225                 230                 235                 240

Val Asp Val Pro Ala Val Ala Val Pro Ala Arg Gln Ala Gly Lys Asp
                245                 250                 255

Leu Val Leu Leu Ile Glu Gly Ile Glu Tyr Asp Pro Gln Ile Asn Asn
            260                 265                 270

Lys Phe Asp Val Val Ile Asn Val Ala Arg Glu Asp Ala Ala Arg Val
        275                 280                 285

Gly Pro Lys Asp Ser Glu Tyr Ala Gly Ser Phe Ser Ala Val Pro Ser
    290                 295                 300

Ser Asn Ala Ala Gly Gly Thr Leu Val Gly Lys Phe Thr Leu Ala Leu
305                 310                 315                 320

Asp Gly Val Leu Ala Asp Leu Gly Leu Ala Gly Ala Ser Ala Val Asp
                325                 330                 335

Ile Val Leu Val Pro His Thr Glu Gly Glu Ile Lys Leu Tyr Leu Pro
            340                 345                 350

Pro Thr Ile Glu Asn Ala
        355
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<210> 39
<211> 2173
<212> DNA
<213> Zea mays

<400> 39
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cgtccaagaa gaccaccgtc gccaggttcc ggcgccgcac ggcgacgtgc agggccagca 180
gcggcggtgg cggtggccgg ggcggcgaaa atgatggcct cctttggctg ccccggcggg 240
acgtgatgct caacggcctg tccagtgtcg ccgccgggct cgcctggtac ccgggcgtcg 300
cgtccggcgc ggatgcggtg tgcaccaggg ccgacaaggt gaacgagaag accgtgcagt 360
gcacggaccc ggccgggcag cttccgtgcc ctctggtgtc gccgacggac cccgtggact 420
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accaggagaa gtacaaggag gccgtcgcga agatgaaggc gctaccggaa gagaacccgc 540
tgagcttcgc ggcccaggcg gccatccacc aggcttactg cgacgcctac tacaagtacg 600
acccgacggc caaggacgcg ccgttcgacg tgcacttctc gtggatcttc gcgccgtggc 660
accgcatgta catctacttc tacgagcgcg ccctcgggca gctcatcggc gacgacacct 720
tcgcgctgcc gttctggaac tgggacacgc cggccggcat ggtggtgccg ccactcttca 780
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cggccgtgcc tgtgccggcc aaggacccgg ggaaggagca gctgctggtg atcgagggca 1620
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agccaatggt agattctaag gaataaataa cattgttatg aatgatatgg ttatgtttta 2160
gagactaatt gcg 2173

<210> 40
<211> 613
<212> PRT
<213> Zea mays

<400> 40
Met Ala Ser Ala Cys Ala Thr Ser Ile Pro Leu Val Ser Ala Pro Ser
1 5 10 15

Ala Cys Pro Ser Lys Lys Thr Thr Val Ala Arg Phe Arg Arg Arg Thr
20 25 30

Ala Thr Cys Arg Ala Ser Ser Gly Gly Gly Gly Gly Arg Gly Gly Glu
35 40 45

```
Asn Asp Gly Leu Leu Trp Leu Pro Arg Arg Asp Val Met Leu Asn Gly
     50                  55                  60

Leu Ser Ser Val Ala Ala Gly Leu Ala Trp Tyr Pro Gly Val Ala Ser
 65                  70                  75                  80

Gly Ala Asp Ala Val Cys Thr Arg Ala Asp Lys Val Asn Glu Lys Thr
                 85                  90                  95

Val Gln Cys Thr Asp Pro Ala Gly Gln Leu Pro Cys Pro Leu Val Ser
            100                 105                 110

Pro Thr Asp Pro Val Asp Phe Lys Pro Glu Ser Lys Val Thr Arg Ile
        115                 120                 125

Arg Gln Pro Val His Leu Leu Ser Arg Glu Tyr Gln Glu Lys Tyr Lys
    130                 135                 140

Glu Ala Val Ala Lys Met Lys Ala Leu Pro Glu Glu Asn Pro Leu Ser
145                 150                 155                 160

Phe Ala Ala Gln Ala Ala Ile His Gln Ala Tyr Cys Asp Ala Tyr Tyr
                165                 170                 175

Lys Tyr Asp Pro Thr Ala Lys Asp Ala Pro Phe Asp Val His Phe Ser
            180                 185                 190

Trp Ile Phe Ala Pro Trp His Arg Met Tyr Ile Tyr Phe Tyr Glu Arg
        195                 200                 205

Ala Leu Gly Gln Leu Ile Gly Asp Asp Thr Phe Ala Leu Pro Phe Trp
    210                 215                 220

Asn Trp Asp Thr Pro Ala Gly Met Val Val Pro Pro Leu Phe Lys Asp
225                 230                 235                 240

Ser Met Gly Asn Pro Leu Tyr Asp Pro Asn Arg Asn Pro Ser Asn Val
                245                 250                 255

Asp Ala Leu Val Asp Leu Asp Tyr Leu Asn Asp Arg Asn Ala Glu Pro
            260                 265                 270

Ile Pro Phe Lys Gly Pro Arg Asp Glu Lys Tyr Lys Glu Leu Val Asn
        275                 280                 285

Lys Asn Leu Cys Thr Val Tyr Thr Gln Gln Ile Arg Ser Gly Lys Gly
    290                 295                 300

Ala Glu Ser Phe Leu Gly Glu Lys Tyr Cys Thr Asp Ile Gly Ser Ser
305                 310                 315                 320

Thr Ser Ser Met Gly Ser Leu Glu Arg Met Ala His Thr Ala Val His
                325                 330                 335

Val Trp Val Gly Lys Ala Gly Pro Thr Pro Ser Ser Glu Ala Cys Ser
            340                 345                 350

Ala Ala Thr Gly Gly Phe Pro Asn His Thr Lys Gly Gly Tyr Ser Cys
        355                 360                 365
```

```
Asn Asn Asp Met Gly Phe Leu Gly Ser Ala Gly His Asp Pro Leu Phe
    370                 375                 380

Tyr Ser His His Ser Asn Val Asp Arg Met Trp His Ile Trp Ser Thr
385                 390                 395                 400

Arg Leu Gly Gly Gly Gln Gly Ile Thr Glu Ala Asp Trp Leu Asp Thr
                405                 410                 415

Ser Phe Val Phe Tyr Asp Asp Val Lys Ser Pro Arg Lys Val Arg Ile
            420                 425                 430

Arg Phe Arg Asp Val Leu Asp Thr Arg Asp Leu Gly Tyr Thr Tyr Asp
        435                 440                 445

Ala Glu Ser Asp Lys Asp Leu Pro Trp Leu Arg Cys Lys Ile Ser Ser
    450                 455                 460

Leu Val Pro His Gly Lys Asp Ser Pro Pro Arg Ser Ser Ser Ala Arg
465                 470                 475                 480

Lys Ala Ala Pro Val Phe Pro Leu Ala Leu Thr Lys Gly Gln Val Val
                485                 490                 495

Glu Val Pro Ala Val Pro Val Pro Ala Lys Asp Pro Gly Lys Glu Gln
            500                 505                 510

Leu Leu Val Ile Glu Gly Ile Glu Tyr Asp Pro Gln Ala Asn Asn Lys
        515                 520                 525

Phe Asp Val Ala Ile Asn Leu Pro Ala Asp Lys Ala Leu Gln Val Gly
    530                 535                 540

Pro Gln Tyr Lys Glu Tyr Ala Gly Ser Phe Ala Val Val Pro Gly Ser
545                 550                 555                 560

Gly Ala Gly Lys Thr Arg Lys Val Lys Leu Ser Leu Cys Ile Thr Glu
                565                 570                 575

Val Leu Phe Asp Ile Asp Ala Asp Gly Asp Lys Thr Val Asp Val Val
            580                 585                 590

Ile Val Pro Arg Thr Asn Ala Lys Ile Thr Leu Asn Ala Arg Pro Thr
        595                 600                 605

Ile Lys Asn Arg Asn
    610
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<210> 41
<211> 409
<212> DNA
<213> Zea mays

<220>
<221> unsure
<222> (409)
<223> n = a, c, g or t

<400> 41
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ggcgactgct atcgccccga caccctctgc atgcccatcc acggttccca agaacaagaa 120
gaatgctgcc ggccggcggc ggcgcacatt gcagtgcagg gccagcggcc ggcggggcga 180
cgacgaagac agccgcctcc tctggctgcc ccggcgggaa gtgctgaccg gtctgggcgg 240
cgtggccgcc agcttcgtcg ggtacccgga tctggcttcc atcgccctgg aagcgaaccc 300
cgtggagagc tgccggcggg gcgagaaggt gacggagaag ctggtggagt gctcggaccc 360
gaacagagac ttcccgtgcc cgccggcgtc acgggtcccc atcgtggan 409

<210> 42
<211> 123
<212> PRT
<213> Zea mays

<400> 42
Met Ala Thr Ala Ser Ala Ala Ser Ser Phe Leu Val Pro Ala Thr Ala
1 5 10 15

Ile Ala Pro Thr Pro Ser Ala Cys Pro Ser Thr Val Pro Lys Asn Lys
20 25 30

Lys Asn Ala Ala Gly Arg Arg Arg Arg Thr Leu Gln Cys Arg Ala Ser
35 40 45

Gly Arg Arg Gly Asp Asp Glu Asp Ser Arg Leu Leu Trp Leu Pro Arg
50 55 60

Arg Glu Val Leu Thr Gly Leu Gly Gly Val Ala Ala Ser Phe Val Gly
65 70 75 80

Tyr Pro Asp Leu Ala Ser Ile Ala Leu Glu Ala Asn Pro Val Glu Ser
85 90 95

Cys Arg Arg Gly Glu Lys Val Thr Glu Lys Leu Val Glu Cys Ser Asp
100 105 110

Pro Asn Arg Asp Phe Pro Cys Pro Pro Ala Ser
115 120

<210> 43
<211> 497
<212> DNA
<213> Glycine max

<220>
<221> unsure
<222> (325)
<223> n = a, c, g or t

<220>
<221> unsure
<222> (397)
<223> n = a, c, g or t

<220>
<221> unsure
<222> (411)
<223> n = a, c, g or t

<220>
<221> unsure
<222> (422)

<223> n = a, c, g or t

<220>
<221> unsure
<222> (438)
<223> n = a, c, g or t

<220>
<221> unsure
<222> (441)
<223> n = a, c, g or t

<220>
<221> unsure
<222> (453)
<223> n = a, c, g or t

<220>
<221> unsure
<222> (463)
<223> n = a, c, g or t

<220>
<221> unsure
<222> (467)
<223> n = a, c, g or t

<220>
<221> unsure
<222> (477)
<223> n = a, c, g or t

<220>
<221> unsure
<222> (487)
<223> n = a, c, g or t

<220>
<221> unsure
<222> (489)
<223> n = a, c, g or t

<400> 43
gacctagact acaacggcgt tgaagaccaa tcctcaacac aagaacaaat atcaaccaat 60
ctcaacacca tgtaccggca actggtgtca agttcaaaga ctccaacgct cttcttcggt 120
agcccttacc gtgcaggaga agatagtgat cccggtggtg gcactgtgga gaacattcct 180
cacggtccgg tccatatatg gaccggtgat aacacacaac ctaactttga ggacatgggg 240
actctctatt ctgctgctag agaccctatt ttctattctc accacgctaa tgtggataga 300
atgtggtcca tatggaaaac tcttngagga aagagagtga catcaaagac cctgattgtt 360
ggaatctggg ttctttctac gatgagaaca agaatcntgt cgtgtgaggt naggattgtc 420
tngtactaga agcttgantg ntaccaaatg atntgtccgt ggnaaancta gccaaancgg 480
tttcgangng gtcaaga 497

<210> 44
<211> 112
<212> PRT
<213> Glycine max

<220>
<221> UNSURE

<222> (109)
<223> Xaa = any amino acid

<400> 44
Asp Leu Asp Tyr Asn Gly Val Glu Asp Gln Ser Ser Thr Gln Glu Gln
1 5 10 15

Ile Ser Thr Asn Leu Asn Thr Met Tyr Arg Gln Leu Val Ser Ser Ser
20 25 30

Lys Thr Pro Thr Leu Phe Phe Gly Ser Pro Tyr Arg Ala Gly Glu Asp
35 40 45

Ser Asp Pro Gly Gly Gly Thr Val Glu Asn Ile Pro His Gly Pro Val
50 55 60

His Ile Trp Thr Gly Asp Asn Thr Gln Pro Asn Phe Glu Asp Met Gly
65 70 75 80

Thr Leu Tyr Ser Ala Ala Arg Asp Pro Ile Phe Tyr Ser His His Ala
85 90 95

Asn Val Asp Arg Met Trp Ser Ile Trp Lys Thr Leu Xaa Gly Lys Arg
100 105 110

<210> 45
<211> 713
<212> DNA
<213> Glycine max

<220>
<221> unsure
<222> (579)
<223> n = a, c, g or t

<220>
<221> unsure
<222> (618)
<223> n = a, c, g or t

<400> 45
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cgtctaaaaa acctagcaaa gcaacaaaac ggcgtcatgc ttgggaagta gcatgcaatg 120
gtaaccctag aaataggagg gacattctga tcggccttgg aggactctat ggtgctacaa 180
caagtctcac aagtaacaac actggttctg catttggtgc ttcattgtcg cctccagatc 240
caactaactg cgttcaaccg gacccagaaa aagacccttt ttgcccacca ccccccttcaa 300
agactacgag ctccctccac acgatgacaa gacattaccc cttcgaatta gaccaagctg 360
ctcatttggt cactgatgat tacatagcca agtacgagga agccgtgagg cgcatgcaag 420
accttccacc tgatgatcct cgcagtttca tgcaacaagc caatgtccac cgtgcctact 480
gcgatggtcc cggctatatc aaaagggttc gctgactaca agcttgacgt tcacggtcct 540
ggatatcctt ccctgggacg ctggtactcc atttctaana aaaacctggg aagatgatcg 600
atgacccact tcgctctncg ttttggaacg ggacaatccc gccggatgag atcctcccat 660
ttcacaagac aaattcactc tctacgacga acacaagaat acgttaatgt taa 713

<210> 46
<211> 162
<212> PRT
<213> Glycine max

<400> 46

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Ser Leu Leu Asn Leu Ser Ala Ser Ile Pro Ile Ser Ser Ser Val Cys
  1               5                  10                  15

Met Phe Pro Pro Ser Lys Lys Pro Ser Lys Ala Thr Lys Arg Arg His
             20                  25                  30

Ala Trp Glu Val Ala Cys Asn Gly Asn Pro Arg Asn Arg Arg Asp Ile
         35                  40                  45

Leu Ile Gly Leu Gly Gly Leu Tyr Gly Ala Thr Thr Ser Leu Thr Ser
     50                  55                  60

Asn Asn Thr Gly Ser Ala Phe Gly Ala Ser Leu Ser Pro Pro Asp Pro
 65                  70                  75                  80

Thr Asn Cys Val Gln Pro Asp Pro Glu Lys Asp Pro Phe Cys Pro Pro
                 85                  90                  95

Pro Pro Ser Lys Thr Thr Ser Ser Leu His Thr Met Thr Arg His Tyr
            100                 105                 110

Pro Phe Glu Leu Asp Gln Ala Ala His Leu Val Thr Asp Asp Tyr Ile
        115                 120                 125

Ala Lys Tyr Glu Glu Ala Val Arg Arg Met Gln Asp Leu Pro Pro Asp
    130                 135                 140

Asp Pro Arg Ser Phe Met Gln Gln Ala Asn Val His Arg Ala Tyr Cys
145                 150                 155                 160

Asp Gly
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